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(54) Title: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND BIOSENSORS OF CHEMICAL SENSANTS

(57) Abstract: The use of sensory G protein-coupled receptors that recognize chemical sensants, particularly those involving olfactory and taste receptors; polypeptide fragments and mutants thereof; classes of such receptors; polynucleotides encoding such receptors, fragments and mutants thereof, and representatives of receptor classes; genetic vectors including such polynucleotides; and cells and non-human organisms engineered to express such receptor complexes, fragments and mutants of an olfactory or taste receptor, and representatives of receptor classes to simulate sensory perception of odorants and tastants is described. The use of such products as a biosensor or a components thereof to detect, identify, measure, or otherwise process the event of binding between the receptor and its cognate ligand (*i.e.*, chemical sensant) is also described. The invention has application, for example, in the design and formulation of odorant and tastant compositions.

Cross Reference to Related Application

Background of the Invention

The invention relates to the use of sensory G protein-coupled receptor complexes that recognize chemical sensants, particularly those involving olfactory and taste receptors; polypeptide fragments and mutants thereof; classes of such receptors; polynucleotides encoding such receptors, fragments and mutants thereof, and representatives of receptor classes; genetic vectors including such polynucleotides; and cells and non-human organisms engineered to express such receptor complexes, fragments and mutants of an olfactory or taste receptor, and representatives of receptor classes to simulate sensory perception of odorants and tastants. The invention also relates to the use of such products as a biosensor or component thereof to detect, to identify, to measure, or otherwise process the event of binding between the receptor and its cognate ligand (*i.e.*, chemical sensant). The invention has application, for example, in the design and formulation of odorant and tastant compositions.

The olfactory and taste systems provide sensory information about the chemical environment. Olfactory receptors and taste receptors recognize, respectively, "odorants" and "tastants," collectively referred to as "sensants" or "sensory receptor ligands" herein. A "primary" sensant is an odorant or tastant ligand that substantially binds to sensory receptors with a ligand-binding site of a single amino acid sequence. Olfactory and taste receptors belong to the superfamily of seven-transmembrane guanyl nucleotide-binding proteins: such receptors are, however, also recognized as distinct families, or sub-genuses, of olfactory or taste

receptors (see Raming *Nature* 361:353, 1993). These receptors control diverse physiological functions such as media-ting signaling from an external chemical stimulus across the membrane containing the receptor into a cell, endocrine function, exocrine function, heart rate, lipolysis, and carbohydrate metabolism. Thus, the
5 dissection of these diverse functions into component signals is needed.

But the complexities of sensory perception of chemical sensants prevent easy translation of the olfaction and taste systems to a machine sensor. For example, U.S. Patent Nos. 5,675,070; 5,918,257; 5,928,609; and 6,085,576 disclose machine sensors that use various chemistries, but they do not take advantage of the specificity of
10 olfactory and taste receptors for their cognate ligands to produce a biosensor.

WO 00/15269 discloses methods and apparatus for odor reproduction. The total affinities of a specific odorant with a group of receptors was called the affinity fingerprint of the odorant. This odorant fingerprint was represented by a vector of affinity values. It was proposed to repro-duce an arbitrary odor by inputting its sensed
15 odorant fingerprint into a device, which has a palate of predetermined odorants and produces a composite odor using predetermined odorant finger-prints by minimizing the difference between vectors representing the sensed odorant fingerprint and the predetermined odorant fingerprints. This reference, however, does not teach or suggest the human olfactory receptors disclosed herein.

20 WO 00/70343 discloses biosensors and sense replication systems using G-protein coupled receptors (GPCR). It was proposed to mimic the response of the G-protein signal transduction system by detecting the affinity of a stimulus to a plurality of GPCR, codifying such information into electronic signals, and reproducing the stimulus by converting the codified information into a combination of stimulant
25 entities. But this reference also does not teach or suggest the human olfactory receptors disclosed herein.

WO 01/27158 discloses olfactory receptors and their use to determine the correspondence between individual odorant receptors and particular odors. It was proposed that the interactions between an odor and olfactory receptors can be used to
30 represent the odor and to re-create it. This reference, however, does not teach or suggest the human olfactory receptors disclosed herein.

Dissecting the function of sensory receptors by binding sensory receptors of a clone of cells expressing a single sensory receptor gene, fragmentation of sensory

receptors to provide ligand-binding or signal-transducing domains thereof, and construction of fusion sensory receptor proteins will separate the diverse physiological functions associated with sensory perception at the level of ligand-receptor binding. Furthermore, novel "primary sensants" that are identified and isolated by the methods described herein may be used to further define the function of the cognate sensory receptor by uniquely enhancing or, in the alternative, blocking stimulation of sensory receptors with a single ligand-binding domain.

The present invention addresses the need for better understanding of these ligand-receptor interactions by using a large set of identified sensory receptors. Even if the receptor set used is incomplete (*i.e.*, a partial set of all sensory receptors encoded in the genome), a large number of sensants will be detected. Moreover, redundancy in the chemical structures recognized by the sensory receptors or combinatorial processing of signals from different sensory receptors would allow broad coverage of chemically diverse sensants (*e.g.*, by selection of a representative class of sensory receptors). Also provided are, *inter alia*, methods for utilizing such sensory receptors and biosensors to simulate sensory perception. To analyze ligand-receptor interactions and their effects on cell signaling and the processing of those signals in sensory perception, specific sensants and their cognate receptor complexes are detected, identified, and measured under binding conditions. Fragrances and flavorings can be detected, identified, measured, and/or custom designed by the methods herein described. In addition, drugs that incorporate artificial odors and/or tastes can be formulated.

Summary of the Invention

Large gene families encoding mammalian olfactory G-protein-coupled receptors (OLFR) and mammalian taste G-protein-coupled receptors (TASR) are known in the prior art or are disclosed herein. An object of the invention to provide fragments and variants of such OLFRs and TASRs which retain odorant- or tastant-binding activity, respectively. The large number of sensory receptors that are made available herein and now amenable to manipulation raises the confidence that a substantially complete, or at least functional, repertoire of sensory receptors is provided.

It is an object of the invention to provide nucleic acid sequences or molecules that encode such sensory receptors, or fragments or variants thereof. Another object is to provide expression vectors which include nucleic acid sequences that encode such sensory receptors, or fragments or variants thereof. It is yet another object of the invention to provide human or non-human cells which functionally express at least one of such sensory receptors, or fragments or variants thereof. Still another object is to provide sensory receptor fusion proteins or other polypeptides which include at least a fragment of at least one of such sensory receptors. In particular, fusions with reporter molecules or other heterologous amino acid sequences may maintain the original ligand-properties while changing the signaling properties to allow easier detection of sensant binding to the receptor (*e.g.*, change in fluorescent signal). Moreover, chimeric proteins or other polypeptides with altered ligand-binding and/or signaling properties can be made from two or more different sensory receptors by mixing domains.

The invention provides methods for representing the sensory perception of one or more chemicals (*e.g.*, a primary sensant or mixture thereof) and/or for predicting the sensory perception of one or more chemicals in a mammal (*e.g.*, human) using the aforementioned products. Given a known member of a ligand-receptor binding pair, one or both members of the pair (*i.e.*, ligand, receptor, or both) may be detected, identified, and/or measured under binding conditions.

Novel molecules or combinations of molecules which elicit a desired and predetermined sensory perception in a mammal (*e.g.*, human) can be generated by determining a value of sensory perception in a mammal for a known molecule or combination thereof; determining a value of sensory perception in a mammal for one or more unknown molecules or combinations thereof; comparing the value of sensory perception in a mammal for one or more unknown compositions to the value of sensory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined sensory perception in a mammal; and mixing two or more unknown molecules or combinations thereof to form a molecule or combination thereof that elicits a predetermined sensory perception in a mammal. The combining step yields a single molecule or a combination thereof that elicits a predetermined sensory perception in a mammal. In particular, primary odorants that uniquely bind to olfactory receptors with a single

ligand-binding domain may be such novel molecules. Variants thereof may be used (1) to enhance stimulation of a limited response by olfactory receptors with a single ligand-binding domain or (2) to block stimulation of olfactory receptors with a single ligand-binding domain to reduce or inhibit olfactory perception. An alternative method for identifying primary odorants is to identify the mutated receptors in genetic anosmias because that odorant would be expected to be recognized by only one or a few olfactory receptors affected by the mutation.

Detailed Description of the Invention

10 Perception of Chemical Sensants

U.S. Patent No. 5,691,188 describes how upon binding of ligand to receptor, the receptor presumably undergoes a conformational change leading to activation of the G protein. The G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $G\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $G\beta\gamma$ complex. When a $G\alpha\beta\gamma$ complex operatively associates with an activated G protein coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of disso-ciation of the bound $G\alpha$ subunit from the $G\alpha\beta\gamma$ complex increases. The free $G\alpha$ subunit and $G\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell. A high-resolution X-ray crystal structure is available for rhodopsin, a guanyl nucleotide binding protein, has been solved (Palczewski *et al.*, *Science* 289:739, 2000). Using this structure, the portions of the amino acid sequence of sensant receptors that are responsible for ligand binding can be identified.

30

Sensory Perception - Olfaction

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel *Sci. Amer.* 273:154, 1995). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer *Semin. Cell Biol.* 5:25, 1994). The human genome contains thousands of genes
5 that encode a diverse repertoire of olfactory receptors (Rouquier *Nat. Genet.* 18:243, 1998; Trask *Hum. Mol. Genet.* 7:2007, 1998). An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that sensory receptors belong to a
10 multigene family with over a thousand members, and the odorant receptors number at least 500 to 1,000. Moreover, each sensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it
15 expresses.

Sensory Perception - Taste

Mammals are believed to have five basic taste modalities: sweet, bitter, sour, salty, and umami (the taste of monosodium glutamate). See, e.g., Kawamura *et al.*,
20 *Introduction to Umami: A Basic Taste* (1987); Kinnamon *et al.*, *Ann. Rev. Physiol.*, 54:715, 1992; Lindemann, *Physiol. Rev.*, 76:718, 1996; Stewart *et al.*, *Am. J. Physiol.*, 272:1, 1997. Numerous physiological studies in animals have shown that taste receptor cells may selectively respond to different chemical stimuli. See, e.g., Akabas
25 *et al.*, *Science*, 242:1047, 1988; Gilbertson *et al.*, *J. Gen. Physiol.*, 100:803, 1992; Bernhardt *et al.*, *J. Physiol.*, 490:325, 1996; Cummings *et al.*, *J. Neurophysiol.*, 75:1256, 1996.

In mammals, taste receptor cells are assembled into taste buds that are distributed into different papillae in the tongue epithelium. Circumvallate papillae, found at the very back of the tongue, contain hundreds, e.g., mice, to thousands, e.g.,
30 human, of taste buds. By contrast, foliate papillae, localized to the posterior lateral edge of the tongue, only contain dozens to hundreds of taste buds. Moreover, fungiform papillae contain only a single or a few taste buds, and are at the front of the tongue.

AC010814, AC018700, AC021304, AC008620, AC011537, AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, AP001803, AP001804, AL353767, AP001884, AC026083, AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, AP002826, AL359636, AL391534, AC055731, AC076959, AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes. Similarly, genes encoding five and thirty-six (36) distinct, novel human T1R and T2R taste receptors, respectively, have been identified in genome sequence databases.

Alternatively, nucleic acids encoding the sensory receptors and other related polypeptides can be isolated from a variety of sources, genetically engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 00/35374, which is herein incorporated by reference in its entirety.

These nucleic acids provide probes for the identification of cells expressing sensory receptors, as the nucleic acids are specifically expressed in such cells. They can also serve as tools for the generation of sensory topographical maps that elucidate the relationship between cells expressing sensory receptors and sensory neurons leading to particular regions of the brain. Furthermore, the nucleic acids and the polypeptides they encode can be used as probes to elucidate olfactant- or tastant-induced behaviors.

Nucleic acid molecules encoding a sensory receptor comprising a nucleic acid sequence that is at least 75%, 85%, 90%, 95%, or 99% identical to a nucleic acid sequence selected from those known in the prior art or disclosed herein are considered variants. Other nucleic acid molecules comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence at least 75%, 85%, 90%, 95%, or 99% identical to an amino acid sequence selected from those known in the prior art or disclosed herein are also considered variants. Further variants contain amino acid

sequence differences in at most ten, five, four, three, two, or one amino acid residue(s).

Exemplary nucleic acid sequences may be selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID

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 SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510; and SEQ ID NO: 512.

Nucleic acid molecule comprising a nucleic acid sequence that encodes a
 fragment of a polypeptide having an amino acid sequence selected from those known
 in the prior art or disclosed herein; wherein the fragment is at least ten, 20, 30, 50, 70,
 30 100, or 150 amino acid residues in length, are useful as probes, primers, and to
 construct hybrids or chimerae.

Polypeptides comprising an amino acid sequence that is at least 90%, 95%,
 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from those

known in the prior art or disclosed herein are considered variants. Further variants contain amino acid sequence differences in at most ten, five, four, three, two, or one amino acid residue(s). Other polypeptides comprising a fragment of a polypeptide having an amino acid sequence selected from those known in the prior art or disclosed
 5 herein; wherein the fragment is at least 40, 60, 80, 100, 150, 200, or 250 amino acid residues in length, are useful as specific binders of sensants, competitive binders, antigens, and to construct hybrids or chimerae.

Exemplary amino acid sequences may be selected from the group consisting of
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 15 ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ
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 NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235,

- SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

Also provided are methods of screening for modulators, *e.g.*, activators, inhibitors, stimu-lators, enhancers, agonists, and antagonists, of the sensory receptors,

or fragments or variants thereof. Such modulators of signal transduction are useful for pharmacological or genetic modulation of signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of sensory cell activity. These modulator compounds can then be used in the pharmaceutical, food, and cosmetic industries to customize odorants or tastants.

Thus, the invention provides assays for sensory modulation, where the sensory receptors, or fragments or variants thereof, act as direct or indirect reporter molecules for the effect of modulators on signal transduction. Sensory receptors, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo*, and *ex vivo*. In one embodiment, sensory receptors, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g.*, Mistili *et al.*, *Nature Biotech.*, 15:961, 1997). In another embodiment, the sensory receptors, or fragments or variants thereof, can be expressed in host cells, and modulation of signal transduction via sensory receptor activity can be assayed by measuring changes in Ca^{2+} levels.

Methods of assaying for modulators of signal transduction include *in vitro* ligand binding assays using the sensory receptors, or fragments or variants thereof. More particularly, such assays can use the sensory receptors; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G-protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular Ca^{2+} levels; and neurotransmitter release.

The invention also provides for methods of detecting sensory receptor nucleic acid and protein expression, allowing for the investigation of taste transduction regulation and specific identification of sensory receptor cells. The sensory receptors, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying a sensory receptor cells. Sensory receptor cells can be identified using techniques such as reverse transcription and amplification

of mRNA, isolation of total RNA or poly A⁺ RNA, Northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, Western blots, and the like.

A. Identification and Characterization of Sensory Receptors

5 The amino acid sequences of the sensory receptors and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

10 For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as
15 described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window," as used herein, includes reference to a segment of
20 any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment
25 of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443, 1970, by the search for similarity method of Pearson & Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and
30 TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J Mol. Biol.* 215:403, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J. Mol. Biol.* 215:403, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-called "tree" or "dendrogram" showing the clustering relationships used to create the alignment (see, e.g., Figure 2). PILEUP uses a simplification of the progressive

alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351, 1987. The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151, 1989. The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, e.g., version 7.0 (Devereaux *et al.*, *Nucl. Acids Res.* 12:387, 1984) encoded by the genes were derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the olfactory receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative sensory receptor proteins generally having lengths of about 300 to about 400 amino acid residues that contain seven transmembrane domains, as predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the 256 sensory receptors identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all 256 sequences contain very close matches to the following consensus amino acid motifs (Mombaerts, 1999; Pilpel, 1999): LHTPMY in intracellular loop 1, MAYDRYVAIC at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5,

FSTCSSH in the beginning of transmembrane domain 6, and PMLNPF in transmembrane domain 7. Combination of all the above mentioned structural features of the 256 genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

5 As noted above, complete or partial sequences of numerous human and other eukaryotic sensory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human sensory receptors, which suggests their different specificity in sensant recognition. Therefore, these novel sensory receptors and their genes can be used, alone or in combination
10 with known sensory receptors, in developing detection systems and assays for chemically distinct types of sensants not recognized by the known sensory receptors, as well as for diagnostic and research purposes.

B. Definitions

The terms "purified," "substantially purified," and "isolated" as used herein
15 refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the
20 compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or
25 concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or
30 proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

The terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (e.g., specific degenerate oligonucleotide primer pairs) for amplifying (e.g., by polymerase chain reaction, PCR) naturally expressed (e.g., genomic or mRNA) or recombinant (e.g., cDNA) nucleic acids of the invention (e.g., sensant-binding sequences of the invention) *in vivo* or *in vitro*.

The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and taste receptors each belong to this super-family. Seven-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

The term "expression vector" refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, *i.e.*, drive only transient expression in a cell. The term includes recombinant expression "cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated sensory, particularly olfactory or taste, receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of vectors that incorporate the amplified sensant-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding a sensory receptor.

The term "nucleic acid" or "nucleic acid sequence" refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded form. The term encompasses nucleic acids, *i.e.*, oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like

structures with synthetic backbones, *see e.g., Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Anti-sense Strategies*, Annals of the N.Y. Academy of Sciences, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan (1993) *J. Med. Chem.* 36:1923-1937; *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata (1997) *Toxicol. Appl. Pharmacol.* 144:189-197; Strauss-Soukup (1997) *Biochemistry* 36:8692-8698; Samstag (1996) *Antisense Nucleic Acid Drug Dev* 6:153-156.

The term sensory receptor "ligand-binding region" refers to sequences derived from a sensory receptor that substantially incorporates transmembrane domains II to VII (TM II to VII). The domain may be capable of binding a sensant.

The terms "conservative variant" or "analog" or "mimetic" refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the poly-peptide's (the conservative variant's) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, etc.) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing function-ally similar amino acids are well known in the art.

For example, one exemplary guideline to select conservative substitutions includes (original residue followed by exemplary substitution): Ala/Gly or Ser; Arg/Lys; Asn/Gln or His; Asp/Glu; Cys/Ser; Gln/Asn; Gly/Asp; Gly/Ala or Pro; His/Asn or Gln; Ile/Leu or Val; Leu/Ile or val; Lys/Arg or Gln or Glu; Met/Leu or Tyr or Ile; Phe/Met or Leu or Tyr; Ser/Thr; Thr/Ser; Trp/Tyr; Tyr/Trp or Phe; Val/Ile or Leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g., Creighton, Proteins*, W.H. Freeman, 1984; Schultz & Schimer, *Principles of Protein Structure*, Springer-Verlag, 1979). One of skill in the art will appreciate that the above-identified substitutions are not the only possible

conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

5 The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains or sensant-binding domains or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or, is a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity. As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups:

10 a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds.

25 Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH₂- for -C(=O)-NH-), aminomethylene (CH₂-NH), ethylene, olefin (CH=CH), ether (CH₂-O), thioether (CH₂-S), tetrazole (CN₄), thiazole, retroamide, thioamide, or ester (see, *e.g.*, Spatola (1983) in *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, Vol. 7, pp 267-357, "Peptide Backbone Modifications,"

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Marcell Dekker, NY). A polypeptide can also be characterized as a mimetic by containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (e.g., "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, e.g., inducible or constitutive expression of a fusion protein comprising a translocation domain of the invention and a nucleic acid sequence amplified using a primer of the invention.

The term "transmembrane domain" means a polypeptide domain that can completely span the plasma membrane. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below.

C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the sensory receptors, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (e.g., promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, e.g., bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, e.g., Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature. See, e.g., Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I, Theory and Nucleic Acid Preparation*, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, e.g., analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, e.g., fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassay (RIA), enzyme-linked immunosorbent assay (ELISA), immunofluorescent assay, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (e.g., SDS-PAGE),

RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned
5 or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, *e.g.*, polymerase chain reaction, PCR (*PCR Protocols, a Guide to Methods and Applications*, ed. Innis. Academic Press, NY, 1990
10 and *PCR Strategies*, ed. Innis, Academic Press, NY, 1995), ligase chain reaction (LCR) (*see, e.g.*, Wu, *Genomics* 4:560, 1989; Landegren, *Science* 241:1077, 1988; Barringer, *Gene* 89:117, 1990); transcription amplification (*see, e.g.*, Kwoh, *Proc. Natl. Acad. Sci. USA* 86:1173, 1989); and, self-sustained sequence replication (*see, e.g.*, Guatelli, *Proc. Natl. Acad. Sci. USA* 87:1874, 1990); Q Beta replicase
15 amplification (*see, e.g.*, Smith, *J. Clin. Microbiol.* 35:1477, 1997); automated Q-beta replicase amplification assay (*see, e.g.*, Burg, *Mol. Cell. Probes* 10:257, 1996) and other RNA polymerase mediated techniques (*e.g.*, NASBA, Cangene, Mississauga, Ontario); *see also* Berger, *Methods Enzymol.* 152:307, 1987; Sambrook; Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563, 1995.

20 Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Patent No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR
25 primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that, when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the sensant-binding region-coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be
30 translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted sensant-binding domain comprises substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I

and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify sensant-binding regions of olfactory receptor proteins. These domain regions may vary for different sensants, and more particularly odorants; thus, what may be a minimal binding region for one sensant, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane sensory receptor.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL. Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII.

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3'). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify a transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL, encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CA-NGT-3'. Such a degenerate primer can
5 be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and
10 is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g., Rose, Nucl. Acids Res.* 26:1628, 1998; Singh, *Biotechniques* 24:318, 1998).

Means to synthesize oligonucleotide primer pairs are well known in the art.
15 "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition.
20 Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res.* 25:4866, 1997. Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol.* 5:950, 1998). For example, two degenerate bases can
25 be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, Proc. Natl. Acad. Sci. USA* 95:4258, 1998). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine, 3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, *see*
30 above). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-
3' and
5'-
5 GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-
3'.
(b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-
3' and
10 5'-
GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-
3'.
(c) 5'-
GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)
GG-3' and
15 5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)
TT(C/T)(C/T)T-3'.

Nucleic acids that encode ligand-binding regions of olfactory receptors are generated by amplification (e.g., PCR) of appropriate nucleic acid sequences using degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, e.g., olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (see, e.g., Buiakova, *Proc. Natl. Acad. Sci. USA* 93:9858, 1996). Shirley, *Eur. J. Biochem.* 32:485, 1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211, 1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, e.g.,

antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260, 1999), describes differentiated olfactory receptor-expressing cells in culture that respond to odorants, as measured by an influx of calcium.

5 Hybrid protein-coding sequences comprising nucleic acids sensory receptors fused to the translocation sequences described herein may be constructed. Also provided are hybrid receptors comprising the translocation motifs and ligand-binding domains of sensory receptors. These nucleic acid sequences can be operably linked to transcriptional or translational control elements, *e.g.*, transcription and translation
10 initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can
15 also be used to express the fusion polypeptide receptor, including, *e.g.*, a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227, 1998). Receptor genes are normally expressed in a small subset of
20 neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

 Fusion proteins, either having C-terminal or, more preferably, N-terminal
25 translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized
30 metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g., Ottavi, Biochimie* 80:289, 1998), subtilisin protease recognition motif (*see, e.g., Polyak, Protein Eng.* 10:615, 1997); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a nucleic acid sequence encoding a polypeptide linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g., Williams, Biochemistry* 34:1787, 1995), and an amino terminal translocation domain. The histidine residues facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature, *see, e.g., Kroll, DNA Cell. Biol.* 12:441, 1993).

Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent literature. *See, e.g., Roberts, Nature* 328:731, 1987; Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10, 1995; Sambrook; Tijssen; Ausubel. Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (*e.g., episomal expression systems*). Selection markers can be incorporated into expression cassettes and vectors to confer a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (*e.g., chloramphenicol, kanamycin, G418, bleomycin, hygromycin*) or herbicide resistance (*e.g., chlorosulfuron or Basta*) to permit selection of those cells transformed with the desired DNA sequences (*see, e.g., Blondelet-Rouault, Gene* 190:315, 1997; Aubrecht, *J. Pharmacol. Exp. Ther.* 281:992, 1997). Because

selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

A chimeric nucleic acid sequence may encode a sensant-binding domain within any 7-transmembrane polypeptide. Seven-transmembrane receptors belong to a superfamily of trans-membrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-trans-membrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains (e.g., TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969, 1999; Rost, *Protein Sci.* 4:521, 1995. Periodicity detection enhancement and alpha helical periodicity index can be done as by, e.g., Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, see, e.g., Peitsch, *Receptors Channels* 4:161, 1996; Cronet, *Protein Eng.* 6:59, (1993) (homology and "discover modeling"); <http://bioinfo.weizmann.ac.il/>.

The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, e.g., TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (e.g., PCR) from mRNA of or cDNA derived from, e.g., olfactory receptor-expressing neurons or genomic DNA.

Libraries of sensory receptor ligand-binding TM domain sequences can include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, e.g., homology modeling, Fourier analysis and helical periodicity (see, e.g., Pilpel *supra*), as described above. Using this information sequences flanking the seven

domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of, for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the sensory receptors described herein, coupled to additional amino acids representing all or part of another G protein receptor, preferably a member of the 7-transmembrane superfamily. These chimerae can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the 7-transmembrane protein described herein, and the remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand binding domain, an extracellular domain, a transmembrane domain (e.g., one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous CGPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, e.g., green fluorescent protein, β -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to a sensory receptor disclosed herein can be isolated using the nucleic acid probes described above. Alternatively, expression libraries can be used to isolate sensory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against a sensory receptor-derived polypeptide, which also recognize and selectively bind to the sensory receptor homolog.

Also within the scope of the invention are host cells for expressing the sensory receptors, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the sensory receptors, fragments, or variants thereof, the nucleic acid sequence of interest is subcloned into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable prokaryotic and eukaryotic expression systems are well known in the art and described, e.g., in Sambrook *et al.*

Any of the well known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasmid vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g., Sambrook et al.*). It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g., WO 00/06593*, which is incorporated by reference in a manner consistent with this disclosure.

D. Immunological Detection of Sensory Receptor Polypeptides

In addition to the detection of sensory receptor genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect

sensory receptors, e.g., to identify olfactory receptor cells, and variants of sensory receptor family members. Immunoassays can be used to qualitatively or quantitatively analyze the sensory receptors. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

5 1. Antibodies to sensory receptor family members

 Methods of producing polyclonal and monoclonal antibodies that react specifically with a sensory receptor family member are known to those of skill in the art (see, e.g., Coligan, *Current Protocols in Immunology*, 1991; Goding, *Monoclonal Antibodies: Principles and Practice*, 2d ed., 1986; Harlow & Lane, supra; and Kohler & Milstein, *Nature*, 256:495, 1975). Such techniques include antibody preparation by
10 selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (see, e.g., Huse et al., *Science*, 246:1275, 1989; Ward et al., *Nature*, 341:544, 1989).

15 A number of sensory receptor-comprising immunogens may be used to produce antibody specifically reactive with a sensory receptor family member. For example, a recombinant sensory receptor protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, e.g., the conserved motifs that are used to identify members of the sensory receptor family.
20 Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Naturally occurring
25 protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

 Methods of production of polyclonal antibodies are known to those of skill in
30 the art. Mice, hamsters, rats, guinea pigs, rabbits, goats, or chickens is immunized with the protein using an adjuvant (e.g., Freund's adjuvant) and a standard immunization protocol with periodic boosts. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of

reactivity to the sensory receptor. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (see Harlow & Lane, *supra*).

5 Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen are immortalized, commonly by fusion with a myeloma cell (see Kohler & Milstein, *Eur. J. Immunol.*, 6:511, 1976). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, retroviruses, or other
10 methods well known in the art. Colonies arising from single clones of immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate host. Alternatively, one may isolate DNA sequences which encode a
15 monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275, 1989.

Monoclonal antibodies or polyclonal sera are collected and titered against antigen in an immunoassay, for example, a solid phase immunoassay with the antigen
20 immobilized on a solid support. Typically, polyclonal antisera with a titer of 10^4 or greater are selected and tested for their cross reactivity against non-sensory receptor proteins, or even other sensory receptor family members or other related proteins from other organisms, using a competitive binding immuno-assay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a K_d of at least about 0.1
25 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

Once sensory receptor family member specific antibodies are available, individual sensory receptor proteins can be detected by a variety of immunoassay methods. For a review of immuno-nological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed., 1991). Moreover, the
30 immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

2. Immunological binding assays

Sensory receptor proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (see, e.g., U.S. Patent Nos. 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general
5 immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed., 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case a sensory receptor family member or an antigenic subsequence thereof). The antibody (e.g., anti-sensory
10 receptor) may be produced by any of a number of means well known to those of skill in the art and as described above.

Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent
15 may be a labeled sensory receptor polypeptide or a labeled anti-sensory receptor antibody. Alternatively, the labeling agent may be a third moiety, such a secondary antibody, that specifically binds to the antibody/sensory receptor complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding
20 immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (see, e.g., Kronval *et al.*, *J. Immunol.*, 111:1401, 1973; Akerstrom *et al.*, *J. Immunol.*, 135:2589, 1985). The labeling agent can be modified with a detectable moiety, such as biotin, to which
25 another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the
30 incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a. Non-competitive assay formats

Immunoassays for detecting a sensory receptor protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays directly measure the amount of antigen. In one preferred "sandwich" assay, for example, the anti-sensory receptor antibodies are bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the sensory receptor protein present in the test sample. The sensory receptor protein thus immobilized is then bound by a labeling agent, such as a second anti-sensory receptor antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g.*, streptavidin, to provide a detectable moiety.

b. Competitive assay formats

In competitive assays, the amount of sensory receptor protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) sensory receptor protein displaced (competed away) from an anti-sensory receptor antibody by the unknown sensory receptor protein present in a sample. In one competitive assay, a known amount of sensory receptor protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the sensory receptor. The amount of exogenous sensory receptor protein bound to the antibody is inversely proportional to the concentration of sensory receptor protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of sensory receptor protein bound to the antibody may be determined either by measuring the amount of sensory receptor protein present in a sensory receptor/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of sensory receptor protein may be detected by providing a labeled sensory receptor molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known sensory receptor protein is immobilized on a solid substrate. A known amount of anti-sensory receptor antibody is added to the sample, and the sample is then contacted with the immobilized sensory receptor. The amount of anti-sensory receptor antibody bound to the known immobilized sensory receptor protein is

inversely proportional to the amount of sensory receptor protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, sensory receptor proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the sensory receptor polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percentage cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the sensory receptor family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or poly-morphic variant of a sensory receptor family member, to the immunogen protein (*i.e.*, sensory receptor protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to

specifically bind to the polyclonal antibodies generated to a sensory receptor immunogen.

Antibodies raised against sensory receptor conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the sensory receptor family, but not to GPCRs from other families. Polyclonal antibodies that specifically bind to a particular member of the sensory receptor family, can be made by subtracting out cross-reactive antibodies using other sensory receptor family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human T2R01 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OLFR1 or mouse OLFR1.

d. Other assay formats

Western blot (immunoblot) analysis is used to detect and quantify the presence of sensory receptor protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind the sensory receptor protein. The anti-sensory receptor polypeptide antibodies specifically bind to the sensory receptor poly-peptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-sensory receptor antibodies.

Other assay formats include liposome immunoassays (LIA) using liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see Monroe et al., Amer. Clin. Prod. Rev.*, 5:34, 1986).

e. Reduction of non-specific binding

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immo-bilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein

compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

f. Labels

The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immuno-assays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, bio-chemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (e.g., DYNABEADS™, fluorescent dyes (e.g., fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (e.g., ^3H , ^{125}I , ^{35}S , ^{14}C , or ^{32}P), enzymes (e.g., horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (e.g., polystyrene, polypropylene, latex, etc.).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (e.g., biotin) is covalently bound to the molecule. The ligand then binds to another molecules (e.g., streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a sensory receptor protein, or secondary antibodies that recognize anti-sensory receptor.

The molecules can also be conjugated directly to signal generating compounds, e.g., by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone,

etc. Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, see U.S. Patent No. 4,391,904.

Methods for detecting labels are well known. Thus, for example, where the label is a radioactive label, it may be detected using a scintillation counter or with photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluoro-chrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, with photographic film, or using electronic detectors such as charge coupled devices (CCDs) or photomultipliers. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally, simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, aggluti-nation assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian sensory, and more particularly, olfactory receptor of the invention, both *in vitro* and *in vivo* are described below, as are methods and compositions for determining whether a test compound is neurotoxic to an olfactory neuron expressing an olfactory transmembrane receptor polypeptide. Any aspect of cell physiology can be monitored to assess the effect of sensant-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical

stimuli into electrical signals. An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and other cognate G-proteins, and modulation of diverse channels by Gi and other G-proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The sensory receptor protein of the assay will typically be selected from a natural poly-peptide or conservatively modified variant thereof. Generally, the amino acid sequence identity will be at least 75%, 85%, 90%, 95%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of a sensory receptor protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand binding domain, subunit association domain, active site, and the like. Either the sensory receptor protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein.

Modulators of sensory receptor activity can be tested using sensory receptor polypeptides as described above, either recombinant or naturally occurring. Protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1. In vitro binding assays

Sensory perception can also be examined *in vitro* with soluble or solid state reactions, using a full-length sensory receptor-GPCR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a sensory receptor covalently linked to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of a sensory receptor. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises all or part of a sensory receptor polypeptide, as well an additional sequence that facilitates the localization of the

sensory receptor to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein.

Ligand binding to a sensory receptor protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid
5 monolayer, or in vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties. Sensory receptors with large (*e.g.*, approximately 600 amino acid residues) extracellular N-terminal segments. These N-terminal segments are thought to form ligand-binding
10 domains, and are therefore useful in biochemical assays to identify sensory receptor agonists and antagonists. Similar assays have been used with other GPCRs, such as the metabo-tropic glutamate receptors (*e.g.*, Han & Hampson, *J. Biol. Chem.* 274:10008, 1999). These assays might involve displacing a radioactively or fluorescently labeled ligand, and measuring changes in intrinsic fluorescence or
15 changes in proteolytic susceptibility, *etc.*

Receptor-G-protein interactions can also be examined. For example, binding of the G-protein to the receptor or its release from the receptor can be examined. For example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be
20 detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits
25 serves as a criterion of activation.

An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and other cognate G
30 proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor sensant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation, or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the sensory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nano-seconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the sensory receptors of the invention, fluorescence-labeled sensants or auto-fluorescent sensants may be used. Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where \parallel is the intensity of the emission light parallel to the excitation light plane and \perp is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For

example, the Beacon® and Beacon 2000™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley *J. Anal. Toxicol.* 5, 236, 1981 which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$\text{Rotational Relaxation Time} = \frac{3\eta V}{RT}$$

The rotational relaxation time is small (≈ 1 nanosecond) for small molecules (e.g., fluorescein) and large (≈ 100 nanoseconds) for large molecules (e.g., immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3. Soluble and solid state high throughput assays

In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand binding domain, an extracellular domain, a transmembrane domain (e.g., one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous protein to create a chimeric molecule; a sensory receptor protein; or a cell or tissue expressing a sensory receptor protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based *in vitro* assays in a high throughput format, where the domain, chimeric molecule, sensory receptor protein, or cell or tissue expressing the sensory receptor is attached to a solid phase substrate.

In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the taste transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,

describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4. Computer-based assays

5 Yet another assay for compounds that modulate sensory receptor protein activity involves computer assisted drug design, in which a digital or analog processing system is used to generate a three-dimensional structure of a sensory receptor protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a
10 preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, *e.g.*, ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering
15 protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a sensory receptor polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of those described herein, or fragments or variants thereof.

20 The amino acid sequence represents the primary sequence or subsequence of the protein, which encodes the structural information of the protein. At least 10 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino acids) are entered into the computer system from computer keyboards, computer readable substrates that include, but are not limited to, electronic storage media (*e.g.*,
25 magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM), information distributed by internet sites, and by RAM. The three-dimensional structural model of the protein is then generated by the interaction of the amino acid sequence and the computer system, using software known to those of skill in the art.

The amino acid sequence represents a primary structure that encodes the
30 information necessary to form the secondary, tertiary and quaternary structure of the protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent

accessible surfaces, and hydrogen bonding. Secondary energy terms include van der Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

5 The tertiary structure of the protein encoded by the secondary structure is then formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface,
10 or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand binding regions are
15 identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the sensory receptor protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined
20 using energy terms to determine which ligands have an enhanced probability of binding to the protein.

Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of sensory receptor genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and
25 related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used to identify patients having such mutated genes. Identification of the mutated sensory receptor genes involves receiving input of a first nucleic acid or amino acid sequence of a sensory receptor gene, or conservatively modified versions
30 thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once

odorant dependent activation monitored. Control samples (untreated with activators or inhibitors) are assigned a relative sensory receptor activity value of 100. Inhibition of a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electrical potential) of the cell or membrane expressing a sensory receptor protein. One means to determine changes in cellular polarization is by measuring changes in current, and thereby measuring changes in polarization, with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575, 1997). Whole cell currents are conveniently determined using the standard. Other known assays include: assays to measure ion flux using radiolabeled or fluorescent probes such as voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67, 1988; Gonzales & Tsien, *Chem. Biol.*, 4:269, 1997; Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185, 1991; Holevinsky *et al.*, *J. Membrane Biology*, 137:59, 1994). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, Northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+} , IP3, cGMP, or cAMP.

Preferred assays for G-protein coupled receptors include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G-protein coupled receptors as negative or positive controls to assess activity of tested compounds. In assays for identifying modulatory compounds (*e.g.*, agonists,

antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed in the Molecular Probes 1997 Catalog. For G-protein coupled receptors, promiscuous G-proteins such as Gα15 and Gα16 can be used in the
5 assay of choice (Wilkie *et al.*, *Proc. Natl. Acad. Sci.*, 88:10049, 1991). Such promiscuous G-proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*, increases in second messengers such as IP3, which releases intracellular stores of
10 calcium ions. Activation of some G-protein coupled receptors stimulates the formation of inositol triphosphate (IP3) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature* 312:315, 1984). IP3 in turn stimulates the release of intracellular calcium ion stores. Thus, a change in cytoplasmic calcium ion levels, or a change in second messenger levels such as IP3
15 can be used to assess G-protein coupled receptor function. Cells expressing such G-protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to
20 distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and
25 olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (see, *e.g.*, Altenhofen *et al.*, *Proc. Natl. Acad. Sci.*, 88:9868, 1991 and Dhallan *et al.*, *Nature* 347:184, 1990). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior
30 to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*, certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors,

serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, sensory receptor protein activity is measured by expressing a sensory receptor gene in a heterologous cell with a promiscuous G-protein that links the receptor to a phospholipase C signal transduction pathway (see Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995). Optionally the cell line is HEK-293 (which does not naturally express sensory receptor genes) and the promiscuous G-protein is Gal 5 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by measuring changes in intracellular Ca^{2+} levels, which change in response to modulation of the sensory receptor signal transduction pathway via administration of a molecule that associates with a sensory receptor protein. Changes in Ca^{2+} levels are optionally measured using fluorescent Ca^{2+} indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be measured using immunoassays. The method described in Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995, may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159, 1994, may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent No. 4,115,538, herein incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent No. 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing a sensory receptor protein of interest is contacted with a test compound for a sufficient time to

effect any interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent No. 5,436,128, herein incorporated by reference. The reporter genes can be, e.g., chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (see, e.g., Mistili & Spector, *Nature Biotech.* 15:961, 1997).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the sensory receptor protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the sensory receptor protein of interest.

6. Transgenic non-human animals expressing sensory receptors

Non-human animals expressing one or more sensory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of translocation domains in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize

odorants/ligands that can bind to a specific or sets of receptors. Such vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

- 5 Means to infect/express the nucleic acids and vectors, either individually or as libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses.
- 10 When electrodes are located on the olfactory bulb surface it is possible to record stable responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287, 1997). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of
- 15 one turbinate bone or were placed in corresponding positions on four turbinate bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950, 1997; Scott, *J. Neuro-physiol.* 75:2036, 1996; Ezeh, *J. Neurophysiol.* 73:2207, 1995. In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and
- 20 medial surface of the turbinates (*see, e.g.*, Youngentob, *J. Neuro-physiol.* 73:387, 1995). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1, 1991).

- The sensory receptor sequences of the invention can be for example expressed
- 25 in animal nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *Proc. Natl. Acad. Sci. USA* 96:4040, 1999.

- The endogenous olfactory receptor genes can remain functional and wild-type
- 30 (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

- Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97, 1997). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotent embryonic stem (ES) cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53, 1998); Moreadith, *J. Mol. Med.* 75:208, 1997; Tojo, *Cytotechnology* 19:161, 1995; Mudgett, *Methods Mol. Biol.* 48:167, 1995; Longo, *Transgenic Res.* 6:321, 1997; U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries can also be used as reagents to produce "knockout" human cells and their progeny.

F. Modulators

- The compounds tested as modulators of a sensory receptor family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of a sensory receptor gene. Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to screen large chemical libraries by

automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (*e.g.*, in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO),
5 Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such
10 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

15 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a
20 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not
25 limited to, peptide libraries (see, *e.g.*, U.S. Patent No. 5,010,175; Furka, *Int. J. Pept. Prot. Res.* 37:487, 1991; and Houghton *et al.*, *Nature* 354:84, 1991). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.*, WO 91/19735), encoded peptides (*e.g.*, WO 93/20242), random bio-oligomers (*e.g.*, WO 92/00091),
30 benzodiazepines (*e.g.*, U.S. Patent No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci.* 90:6909, 1993), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568, 1992), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer.*

Moreover, a method is provided for simulating a fragrance or flavor sensed by a mammal (*e.g.*, human), comprising: for each of a plurality of sensory receptors, or fragments or variants thereof, ascertaining the extent to which the sensory receptor interacts with the fragrance and/or flavor; and combining a plurality of compounds, each having a previously-determined interaction with one or more of the sensory receptors, in amounts that together provide a stimulation profile that mimics the profile for the fragrance and/or flavor. Interaction of a fragrance and/or flavor with a sensory receptor can be determined using any of the binding or reporter assays described herein. The interactions can be aggregated or a profile generated using known signal processing techniques (*e.g.*, a neural network) as described below. The sensory receptor, or fragments or variants thereof (*e.g.*, fusion proteins with reporters, chimeric proteins) may be expressed in cells; otherwise, ligand-binding domain(s) may be fixed to a substrate (*e.g.*, planar, bead, or fiber) that is solid or porous. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80%, 90%, 95%, 99% or all of the receptors that are substantially stimulated by the fragrance or flavor.

In yet another aspect of the invention, a method is provided in which a plurality of standard compounds are tested against a plurality of sensory receptors, or fragments or variants thereof, to ascertain the extent to which the sensory receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on data storage medium. The method may further comprise providing a desired receptor-stimulation profile for an odor and/or taste; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the odor and/or taste.

A further aspect of the invention is to provide a method for representing sensory perception of a particular odor and/or taste in a mammal (*e.g.*, human), comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is greater than or equal to 5, n is

greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; and generating from the values a quantitative representation of sensory perception. The sensory receptors may be a receptor disclosed herein, or fragments or variants thereof. The representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, or may constitutes a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced sensory receptors, or fragments or variants thereof, with a composition and quantitatively measuring the interaction of the composition with the receptors. The maximum number of taste receptors that are needed to mimic the native repertoire (e.g., about 50) may be less than the maximum number of olfactory receptors that are needed (e.g., about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

It is yet another aspect of the invention to provide a method for predicting the sensory perception in a mammal (e.g., human) generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in the mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is greater than or equal to 5, n is greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; for one or more molecules or combinations of molecules yielding known sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is

greater than or equal to 5, n is greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; for one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal by comparing the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal to the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal. The sensory receptors used in this method may include a receptor disclosed herein, or fragment or variant thereof. The maximum number of taste receptors that are needed to mimic the native repertoire (*e.g.*, about 50) may be less than the maximum number of olfactory receptors that are needed (*e.g.*, about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

Assaying for ligand-receptor binding in a large set of sensory receptors is envisioned to mimic the function of the nose or tongue in sensory perception of chemical sensants. For a set of sensory receptors with a redundancy of ligand-binding domains, the resultant signal is a summation of the interactions of all sensory receptors in the set: none, one, or a few of which have ligand-binding domains that are a perfect fit for the sensant; some of which have ligand-binding domains that are only an imperfect fit for the sensant; and most of which do not significantly bind to the sensant. The individual sensory receptor's binding affinity for sensant varies accordingly. Thus, a suitably large set of ligand-binding domains from sensory receptors will be analogous to any ability of the native repertoire of olfactory or taste receptors to tolerate varying degrees of mismatch between ligand and ligand-binding domain.

The complication of desensitization of sensory receptor signaling will also be avoided by using the invention instead of preparations of nasal or tongue epithelium containing native sensory receptors. For example, the event of binding between ligand and receptor can be separated from more complicated downstream signaling events in the epithelial cells. But the latter events can be reconstituted in the invention by transferring the sensory receptor of interest into appropriate host cells containing an intact and functional signaling pathway.

H. Administration of Novel Sensant Compositions

Sensory modulators can be administered directly to a mammal (*e.g.*, human) for modulation of sensory perception *in vivo*. Administration is by any of the routes normally used for introducing a modulator compound into ultimate contact with the tissue to be treated (*e.g.*, nose or tongue). The olfactory modulators are administered in any suitable manner, optionally with acceptable carriers. Suitable methods of administering such modulators are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route. Acceptable carriers are determined at least in part by the particular components of the composition to be administered (*e.g.*, stabilizing the sensants), as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions of the present invention (*see, e.g., Remington's Pharmaceutical Sciences*, 17th ed. 1985).

The sensory modulators, alone or in combination with other suitable components, can be made into aerosol formulations (*i.e.*, they can be "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichloro-difluoromethane, propane, nitrogen, and the like that may or may not contribute to sensory perception. Other possible formulation include dry or liquid forms, powders or tablets, solutions of polar (*e.g.*, water) or nonpolar (*e.g.*, alcohol) solvents, emulsions or suspensions, creams, gels, lotions, and syrups.

Formulations suitable for administration include aqueous and non-aqueous solutions, isotonic sterile solutions, which can contain antioxidants; buffers,

bacteriostats, and solutes that render the formulation isotonic, and aqueous and non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. In the practice of this invention, compositions can be administered, for example, by orally, topically, intravenously, 5 intraperitoneally, intravesically, or intrathecally. Optionally, the compositions are administered orally or nasally. The formulations of compounds can be presented in unit-dose or multi-dose sealed containers, such as ampules and vials. Solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described. The modulators can also be administered as part of prepared 10 drug, food, or cosmetic. In particular, an un-pleasant odor or taste (e.g., sulfur or bitter, respectively) may not be perceived as such and/or its effects reduced by blocking the binding between sensant ligand and sensory receptor by adding a competitor ligand that blocks binding between cognate ligand and receptor, or inhibiting or reducing signal transduction. In contrast, a pleasant odor or taste can be 15 mimicked or enhanced. Primary sensants are preferred because the subset of activated cells is kept small and the effects limited to projection into a specific region of the brain. But novel olfactants or combinations thereof that bind only a few olfactory receptors (e.g., having less than five different ligand-binding domains) would also be useful.

20 The dose administered to a mammal (e.g., human) should be sufficient to effect a beneficial response in the subject over time. The dose will be determined by the efficacy of the particular sensory modulators employed and the condition of the subject, as well as the body weight or surface area of the area to be treated. The size of the dose also will be determined by the existence, nature, and extent of any adverse 25 side-effects that accompany the administration of a particular compound or vector in a particular subject. In determining the effective amount of the modulator to be administered in a physician may evaluate circulating plasma levels of the sensory modulator, modulator toxicities, and the production of anti-modulator antibodies. In general, the dose equivalent of a modulator is from about 1 ng/kg to 10 mg/kg for the 30 typical mammal. For administration, sensory modulators can be administered at a rate determined by the ED₅₀ of the modulator, and the side-effects of the inhibitor at various concentrations, as applied to the mass and overall health of the mammal. Administration can be accomplished via single or divided doses.

I. Kits

Sensory receptor genes, or fragments or variants thereof are useful tools for identifying cells expressing sensory receptors, for forensics and paternity determinations, and for examining signal transduction in isolated cells. Sensory
5 receptor family member-specific reagents that specifically hybridize to sensory receptor nucleic acids, such as AOFLF1 probes and primers, and sensory receptor specific reagents that specifically bind to a sensory receptor protein, *e.g.*, anti-sensory receptor antibodies are used to examine expression in cells and regulation of signal trans-duction. For example, one or more family member-specific reagents may be
10 used to detect poly-morphisms that are linked to genetic anosmia or to detect allelic exclusion.

Nucleic acid assays for the presence of DNA and RNA for a sensory receptor family member in a sample include numerous techniques are known to those skilled in the art, such as Southern analysis, Northern analysis, dot blots, RNase protection, S1
15 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such as to be available for hybrid-ization within the cell while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*,
20 *Biotechniques*, 4:230-250 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, a sensory receptor protein can be detected with the various immunoassay techniques described above. The test sample is typically compared to both a positive control (*e.g.*, a sample expressing a recombinant sensory
25 receptor protein) and a negative control.

The present invention also provides for kits for screening for novel modulators of sensory receptor family members. Such kits can be prepared from readily available materials and reagents, as well as any of the aforementioned products. For example, such kits can comprise any one or more of the following materials: sensory receptor
30 nucleic acids or proteins, reaction tubes, and instructions for testing sensory receptor activity. Optionally, the kit contains a biologically active sensory receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

Examples

AOLFR1 sequences:

5 MKTFSSFLQIGRNMHQGNQTTTTEFILLGFFKQDEHQNLLFVFLGMYLVTVIGNGLIIVALSID
 TYLHTPMYFLANLSFADISSISNSVPKMLVNIQTKSQSISYESCITQMYFSIVFVIDNLLGTM
 AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIIALHTLLLIQLLFCNHNTPHFFCDLAPLL
 KLSCSDTLINELVLFIVGLSVIHPFTLSFFSYVCIIRAVLRVSSTQGWKAFSTCGSHLTVVLLFY
 GTIVGVYFFPSSTHPEDTDKIGAVLFTVVTMPINPFIYSLRNKDMKGALRKLINRKISSL (SEQ ID
 NO: 1)

10 ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA
 CCATCACTGAATTCATTCTCCTGGGATTTTCAAGCAGGATGAGCATCAAAACCTCCTCTT
 GTGCTTTTCTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTGTGGCTA
 TCAGCTTGGATACGTACCTTCATACCCCCATGTATCTTCTCCTTGCCAATCTATCCTTTGCT
 GATATTTCTCCATTTCCAACCTCAGTCCCCAAATGCTGGTGAATATTCAAACCAAGAGTC
 15 AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTCTGTCATT
 GACAATTTGCTCTTGGGGACCATGGCCTATGACCACTTTGTGGCGATCTGCCACCTCTGA
 ATTATACAATTCTCATGCGGCCCCAGGTTGCGCATTTTGTCTCACAGTCATCTCATGGTTCTC
 AGTAATATTATTGCTCTGACACACACCCCTTCTGCTCATTCAATTGCTCTTCTGTAACCACAA
 CACTCTCCACACTTCTTCTGTGACTTGGCCCCCTGCTCAAACCTGCTCTGTTAGATACAT
 20 TGATCAATGAGCTTGTGTTGTTTATTGTGGGTTTATCAGTTATCATCTTCCCTTTACACTC
 AGCTTCTTTTCTATGTCTGCATCATCAGAGCTGTCTGAGAGTATCTCCACACAGGGAA
 AGTGGAAAGCCTTCTCCACTTGTGGCTCTCACTGACAGTTGTATTACTGTTCTACGGAAC
 CATTGTAGGCGTGTACTTTTCCCTCTCCACTCACCCTGAGGACACTGATAAGATTGGT
 GCTGTCCTATTCACTGTGGTGACCCCATGATAAACCCCTTCATCTACAGCTTGAGGAATA
 25 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTCTTCCCTTTGA (SEQ
 ID NO: 2)

AOLFR2 sequences:

30 MMMVLRNLSMEPTFALLGFTDYPKLQIPLFLVFLLMYVITVVGNLGMIIIIKINPKFHTPMYFFL
 SHLSFVDFCYSSIVTPKLEENLVMAKDSIFYSCMMQYFLSCTAVVTESFLAVMAYDRFVAIC
 NPLLYTVAMSQRLLCALLVAGSYLVGMFGPLVLLCYALRLNFSGPNVINHFFCEYALISVSGS
 DILPHLLLFSFATFNEMCTLLIILTSYVFIVTVLKIRSVSGRHKAFSTWASHLTAITIFHGTLFL
 YCVPNSKNSRQTVKVASVFYTVVNPMLNPPIYSLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:
 3)

35 ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCCACCTTTGCCCTTTTAGGTTTCACAG
 ATTACCCAAAGCTTCAGATTCCTCTCTCCTTGTTTCTGCTCATGTATGTTATCACAGTG
 GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAACCCCAAATTCACACTCCTATGT
 ACTTTTCTTAGTCACTCTCTTTTGTGATTTTGTACTCTTCCACTTGTACTCCCAAGC
 40 TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGCAGTA
 CTTCTGTCTGCACTGCTGTGGTGACAGAGTCTTCTTGTGCTGGCAGTGACAGAGGCTCTGTG
 CGCTTTGTGGCCATCTGCAATCCTCTGCTTTATACAGTGGCCATGTACAGAGGCTCTGTG
 CCCTGCTGGTGGCTGGGTCATCTCTGGGGCATGTTGGCCCCCTTGGTACTCCTTTGTTAT
 GCTCTCCGGTTAAACTTCTCTGGACCTAATGTAATCAACCACTTCTTTGTGAGTATACTGC
 45 TCTCATCTCTGTGTCTGGCTCTGATATACTCATCCCCACCTGCTGCTTTTCAGCTTCGCCA
 CCTTCAATGAGATGTGTACACTACTGATCATCTCACTTCTATGTTTTCATTTTGTGACT
 GTACTAAAAATCCGTTCTGTTAGTGGGCGCCACAAAGCCTTCTCCACTGGGCTCCCAAC
 TGACTGCTATCACCATCTTCCATGGGACCATCTTTCTTTACTGTGTACCAACTCCAA
 AACTCTCGGCAACAGTCAAAGTGGCCTCTGTATTTACACAGTTGTCAACCCCATGCTGA
 50 ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTTCTGGAAGTTAATACA
 TACACAAGTTCCATTTCAGTGA (SEQ ID NO: 4)

AOLFR3 sequences:

55 MLLTDRNTSGTTFLLGFSDPYELQVPLFLVFLAIYNVTVLGNIGLIVIIKINPKLHTPMYFFLSQ
 LSFVDFCYSSIIAPKMLVNLVVKDRITISFLGCVVQFFFFCTFVVTESFLAVMAYDRFVAICNPL
 LYTVDMSQKLCVLLVVGSYAWGVSCSLELTCSALKLCFHGFNTINHFFCEFSLLSLSCSDTYI

NQWLLFFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITIFHGTLFLYCV
PNSKNSRHTVKVASVFYTVVIPMLNPLIYSLRNKDVKDTVTEILDTKVFSY (SEQ ID NO: 5)

5 ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTACCCCTCTTGGGCTTCTCAGATT
ACCCAGAACTGCAAGTCCCACTCTTCCTGGTTTTCTGGCCATCTACAATGTCACTGTGCTA
GGGAATATTGGGTTGATTGTGATCATCAAAATCAACCCCAAACCTGCATACCCCATGTACT
TTTTCTCAGCCAACTCTCCTTTGTGGATTCTGTCTATTCTCCATCATTGCTCCCAAGATG
TTGGTGAACCTTGTGTCAAAGACAGAACCATTTCATTTTTAGGATGCGTAGTACAATTCT
TTTTCTTCTGTACCTTTGTGGTCACTGAATCCTTTTTATTAGCTGTGATGGCCTATGACCGC
10 TTCGTGGCCATTTGCAACCCTCTGCTCTACACAGTTGACATGTCCAGAACTCTGCGTGC
TGCTGGTTGTGGGATCCTATGCCTGGGGAGTCTCATGTTCTTGGAAGTACGTTGCTCTGC
TTTAAAGTTATGTTTTCATGGTTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCCTCAC
TACTCTCCCTTTCTGTCTGTGATACTTACATCAACCAGTGGCTGCTATTCTTTCTTGCCACC
TTTAATGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTCATTGTTGTAACCAT
15 CCTCAAGATGCGTTCAGTCAGTGGGCGCCGCAAAGCCTTCTCCACCTGTGCCTCCACCTG
ACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTTACTGTGTGCCCAACTCCAAAAA
CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCATGTTGAAT
CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC
ACCAAAGTCTTCTCTTACTGA (SEQ ID NO: 6)

20

AOLFR4 sequences:

MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS
LLDVMFSSVVPKVVIVDTLSKSTTISLKGCLTQLFVEHFFGGVGIILLTVMAYDRYVAICKPLHY
TIIMSPRVCCLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIIDHFICDLFQLLTACTDTHILGL
25 LVTLSNGMMCVAFILIASYTVILCSLSYSSKGRHKALSTCSSHLTVVVLFFVPCIFLYMRPV
VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

ATGGAAAATCAAAACAATGTGACTGAATTCATTCTTCTGGGTCTCACAGAGAACCTGGAGC
TGTGGAAAATATTTTCTGCTGTGTTTCTTGTGATGTATGTAGCCACAGTGTGGAAAATCT
30 ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTCACCTATGTATTTTTTTCTTA
CCTTCTTGTCCCTTTTGGATGTCATGTTCTCATCTGTGCTTGCCCCCAAGGTGATTGTAGAC
ACCCTCTCCAAGAGCACTACCATCTCTCTCAAAGGCTGCCTCACCCAGCTGTTTGTGGAGC
ATTTCTTTGGTGGTGTGGGGATCATCCTCCTCACTGTGATGGCCTATGACCGCTACGTGGC
CATCTGTAAGCCCCCTGCACTACACGATCATCATGAGTCCACGGGTGTGCTGCCTAATGGTA
35 GGAGGGGCTTGGGTGGGGGGATTATGCACGCAATGATACAACTTCTCTTCATGTATCAAA
TACCCTTCTGTGGTCCTAATATCATAGATCACTTTATATGTGATTTGTTTCAGTTGTTGACA
CTTGCCTGCACGGACACCCACATCCTGGGCCTCTTAGTTACCCTCAACAGTGGGATGATGT
GTGTGGCCATCTTTCTTATCTTAATTGCGTCCTACACGGTCATCCTATGCTCCCTGAAGTCT
TACAGCTCTAAAGGGCGGCACAAAGCCCTCTCTACCTGCAGCTCCACCTCACGGTGGTTG
40 TATTGTTCTTTGTCCCCTGTATTTTCTTGTACATGAGGCCTGTGGTCACTACCCCATAGAC
AAGGCAATGGCTGTGTGCACTCAATCATCACACCCATGTTAAATCCCTTGATCTATACAC
TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTTGG
CTGGGAAATAA (SEQ ID NO: 8)

45 **AOLFR5 sequences:**

MGKENCTTVAEFILLGLSDVPELRVCLFLLFLLIYGVTLLANLGMIALIQVSSRLHTPMYFFLSH
LSSVDFCYSSIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLLAVMAYDRFVAICNPL
LYTVTMSWKVRVELASCCYFCGTVCSLIHLCLALRIPFYRSNVINHFCDLPVLSLACSDITVN
ETLLFLVATL NESVTIMILTSYLLILTILKMGS AEGRHKAFSTCASHLTAITVFHGT VLSIYCRP
50 SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKEALRKVMGSKIHS (SEQ ID NO: 9)

ATGGGCAAGGAAAACCTGCACCACTGTGGCTGAGTTCAATTCTCCTTGGACTATCAGATGTCC
CTGAGTTGAGAGTCTGCCTCTTCTGCTGTTCTTCTCATCTATGGAGTCACGTTGTTAGCC
AACCTGGGCATGATTGCACTGATTCAAGTCAGCTCTCGGCTCCACACCCCATGTACTTTT
55 TCCTCAGCCACTTGTCTCTGTAGATTCTGCTACTCCTCAATAATTGTGCCAAAAATGTTG
GCTAATATCTTTAACAAGGACAAAGCCATCTCCTTCTAGGGTGCATGGTGCAATTCTACT

TGT TTTGCACTTGTGTGGTCACTGAGGTCTTCTGCTGGCCGTGATGGCCTATGACCGCTTT
 GTGGCCATCTGTAACCTTTTGCTATACACAGTCAACATGTCTTGAAGGTGCGTGTGGAGC
 TGGCTTCTTGCTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCATTTGTGCTTAGCTCTT
 AGGATCCCCCTTCTATAGATCTAATGTGATTAACCACTTTTCTGTGATCTACCTCCTGTCTT
 5 AAGTCTTGCTTGCTCTGATATCACTGTGAATGAGACACTGCTGTTCTGCTGGCCACTTTG
 AATGAGAGTGTACCATCATGATCATCCTCACCTCCTACCTGCTAATTCTCACCACCATCCT
 GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCACCTCACA
 GCTACTACTGTCTTCCATGGAACAGTCCTTTCCATTTATTGCAGGCCAGTTCAGGCAATA
 GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCTATGCTGAACCTC
 10 TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC
 CAAAATTCACCTCTAG (SEQ ID NO: 10)

AOLFR6 sequences:

15 MMASERNQSSPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS
 HSLTDFCFSTVTPKLENLVVEYRTISFSGCIMQFCACIFGVTETFMLAAMAYDRFVAVCK
 PLLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLDLFSCESTFINNFICDHSVIVSASYSOPYIS
 QRLCFIIAIFNEVSSLIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTATITFHGTILFLYCVPNP
 KTSSLIVTVASVFYTVAIPLNPLIYSLRNKDINMFEKLVVTKLIYH (SEQ ID NO: 11)

20 ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTCAG
 AATACCCAGAAATCCAGGTTCCACTCTTTCTGGTTTTCTTGTTCGTCTACACAGTCACTGTA
 GTGGGGAACTTGGGCATGATAATAATCATCAGACTCAATTCAAACTCCATACAATCATGT
 ACTTTTCTTCTAGTCACTTGTCTTACAGACTTCTGTTTTTCCACTGTAGTTACACCTAAA
 CTGTTGGAGAACTTGGTGTGGAATACAGAACCTTCTTCTCTGTTGTCATCATGCAAT
 25 TTTGTTTTGCTTGCATTTTTGGAGTGACAGAACTTTCATGTTAGCAGCGATGGCTTATGAC
 CGTTTTGTGGCAGTTGTAAACCTTGTGTATACCACTATTATGTCTCAGAAAGCTCTGTGC
 TCTTCTGGTGGCTGGTCTTACATGGGGGATAGTGTGCTCCCTGATACTACATATTTT
 CTTCTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTATCTGTGACCACTCTGT
 AATTGTTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATATTGCCA
 30 TATCAATGAGGTGAGCAGCCTAATTATCTGACATCATATAGCTTATTTTCACTACC
 ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACCTTCTCCACCTGTGCCTCCCACC
 TGACAGCCATCACTATCTCCATGGAACCTATCCTTTTCTTACTGTGTTCTCTAATCTCTAAA
 ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA
 ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT
 35 CACCAAATTGATTTACCACTGA (SEQ ID NO: 12)

AOLFR7 sequences:

40 MSYFYRLKLMKEAVLVKLPFTSLPLLQLTSRKS RDMEIKNYSSSTSGFILLGLSSNPQLQKPLF
 AIFLIMYLLAAVGNVLIIPIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFLSETKVISY
 VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLMLLGSCSISHLSL
 FRVLLMSRLSFCASHIHKHFFCDTQPVLKLSGSDTSSSQMVMTETLAVIVTPFLCIIFS YLRIMV
 TVLRIPSAAGKWKAFSTCGSHLTAVALFYGSIYVYFRPLSMYSVVRDRVATVMYTVVTPMLN
 PFIYSLRNKDMKRLKLLQDRIYR (SEQ ID NO: 13)

45 ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTTA
 CATCTCTCCCACTGCTTCTCAAACCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA
 CTACAGCAGCAGCAGCAGGCTTCTCTCTGGGCTCTCTTCAAACCTCAGCTGCAG
 AAACCTCTCTTGGCATCTTCTCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT
 CATCCCGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACTTTTTCTCAGCAACT
 50 TGTCTTTCATGGATATCTGCTTCAACAGTCATAGTGCCTAAGATGCTGGTGAATTTTCTA
 TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTACTTCTTATGGCAT
 TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGGCTGGTGGCCATCTG
 CAACCCCTTACACTATGATGTGGTTATGAAACCAGGCATTGCCTGCTCATGCTATTGGGT
 TCTTGCAGCATCTCCACCTACATTCCTGTTCGCGTGCTACTTATGTCTCGCTTGTCTTT
 55 CTGTGCCTCTCACATCATTAAAGCACTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT
 GCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTTAGCTGTCAATGTGAC

CCCCCTCCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCCT
 CTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCCACCTCACTGCAGTAGCCCT
 TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCTGTCCATGTACTCAGTGGTTAGGG
 ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCCTTCATCTACAG
 5 CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA
 A (SEQ ID NO: 14)

AOLFR8 sequences:

MATSNHSSGAEFILAGLTQRPELQLPLFLLFLGIYVTVVGNLGMIFLIALSSQLYPPVYYFLSH
 10 LSFIDLCYSSVITPKMLNVFVPEENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPLLY
 NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTSCSSTHINEI
 LLFIIGGVNTLATTALVLISYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFFGSITFMYFKPPSS
 TTMEKEKVSSVFYITIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

15 ATGGCTACTTCAAACCAATTCTTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC
 CAGAACTTCAACTGCCACTCTTCCTCCTGTTCCCTGGAATATATGTGGTCACAGTGGTGGG
 GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTACCCTCCAGTGTATTATT
 TTCTCAGTCATTTGTCTTTCATTGATCTCTGCTACTCCTCTGTCTATTACCCTAAGATGCTG
 GTGAACTTTGTTCCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATTT
 20 CTTCTTATTTTTGTAATTGCAGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT
 GTTGCTATCTGTGCGCCCACTGCTTTACAATATTGTCTATGTCCACAGGGTCTGTTCCATAAT
 GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA
 GTGTTGTCATTCTGTAGGTCTCATACGGTCAGTCATTATTTTTGTGATATTCTCCCCTTATT
 GACTCTGTCTTGCTCCAGCACCCACATCAATGAGATTCTGCTGTTTATTATTGGAGGAGTT
 25 AATACCTTAGCAACTACACTGGCGGTCTTATCTCTTATGCTTTCATTTTCTCTAGTATCCT
 TGGTATTCAATCCACTGAGGGGCAATCCAAAGCCTTTGGCACTTGCTAGCTCCCATCTCTTG
 GCTGTGGGCATCTTTTTTGGGTCTATAACATTGATGATTTCAAGCCCCCTTCCAGCACTAC
 TATGGAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT
 CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA
 30 AGGCAGTCATCCTGA (SEQ ID NO: 16)

AOLFR9 sequences:

MLARNNSLVTEFILAGLTDRPEFWQPFFFLFLVIYIVTMVGNLGLITLFLGLNSHLHTPMYYFLFN
 LSFIDLCYSSVFTPKMLMNFVSKKNISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL
 35 LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANIINHYLCDILPLLQLSCTSTYV
 NEVVVLIVVGTNITVPSCITILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY
 SSGSMEQGVFSVFYTNVPMNLPLIYSLRNKDVKVALRKALIKIQRNIF (SEQ ID NO: 17)

40 ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
 CAGAGTTCTGGCAACCCTTCTTTTTCTGTTCTAGTGATCTACATTGTACCATGGTAGGC
 AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTTCTCACCTCCACACACCAATGTACTATT
 CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAATGCTAAT
 GAACTTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC
 TTTCTCTTTTCGTCTATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT
 45 GGCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCA
 CTTTGTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGTTTAG
 ACTCACCTTCTGCAGTGCTAATATCATTAACCATTACTTGTGTGACATACTCCCCCTCCTCC
 AGCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTACTAA
 TATCACGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTTATTGTCAGTACTAGCATTCTTC
 50 ATATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGCTAGCTCTCATGTGATTGC
 TCTGTCTCTGTTTTTGGGTGAGCGGCATTGATGATATTAATAATTTCTTCTGGATCTATGG
 AGCAGGGAAAAGTTTTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCCCCTCATC
 TACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTTCAG
 AGGAGAAATATATTCTAA (SEQ ID NO: 18)

55

AOLFR10 sequences:

5 MLARNNSLVTEFILAGLTDRPEFRQPLFFLFLVIYIVTMVGNLGLILFGLNSHLHTPMYYFLFNL
SFIDLCYSSVFTPKMLMNFVSKKNISYVGCMTQLFFLFFVISECYILTSMA YDRYVAICNPLLY
KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMRLRTFCSANIINHLYCDILPLLQLSCTSTYVN
EVVVLIVVGINIMVPSTILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFM YIKYS
SGSMEQGVSSVFYTNVVPMLNPLIYSLRNKDV KVALRKALIKIQRNIF (SEQ ID NO: 19)

10 ATGCTGGCTAGAAACAACTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCGGGCAACCCCTCTTTTCTGTTTCTAGTGATCTACATTGTCACCATGGTAGGC
AACCTTGGCTTGATCATTCTTTTCGGTCTAAATCTCACCTCCACACACCAATGTACTATT
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCTCTGTTTCACTCCCAAAATGCTAAT
GAACTTTGTATCAAAAAGAATATTATCTCCTATGTTGGGTGCATGACTCAGCTGTTTTCT
TTCTCTTTTTGTCTCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG
15 GCCATCTGTAATCCATTGCTGTATAAGGTCAACCATGTCCCATCAGGTCTGTTCTATGCTCAC
TTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGTGCATGCTTAGA
CTCACCTTCTGCAGTGCTAATATCATCAACCATTACTTGTGTGACATACTCCCCCTCCTCCA
GCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTGTCTCATTGTTGTGGGTATTAAT
ATCATGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTCATTGTCACTAGCATTCTTCA
TATCAAATCCACTCAAGGAAGATCAAAGCCTTCAGTACTTGTAGCTCTCATGCTATTGCT
20 CTGTCTCTGTTTTTGGGTGAGCGGCATTCTATGATATTAATATTCTTCTGGATCTATGGA
GCAGGGAAAAGTTTCTTCTGTTTCTACATAATGTGGTGCCCATGCTCAATCCTCTCATCT
ACAGTTTGAGGAACAAGGATGTCAAAGTGCAGTGAGGAAAGCTCTGATTAATAATTCAGA
GAAGAAATATATTCTAA (SEQ ID NO: 20)

25 AOLFR11 sequences:

MTLRNSSSVTEFILVGLSEPELQLPLFLFLGIYVFTVVGNLGLITLIGINPSLHTPMYYFLFNL
FIDLCYSCVFTPKMLNDFVSEIISYVGCMTQLFFFCFFVNSECYVLVSMAYDRYVAICNPLLY
MVTMSPRVCFLLMFGSYVVGFAAGAMAHTGSMRLRTFCDNSVIDHYLCDVLPPLLQLSCTSTHV
30 SELVFFIVGVITMLSSISIVISYALILSNILCIPSAEGRSKAFSTWGSILAVLFFGSGTFTYLTTS
FPGSMNHGRFASVFYTNVVPMLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)

35 ATGACTCTGAGAAACAGCTCCTCAGTGACTGAGTTTATCCTTGTTGGGATTATCAGAACAGC
CAGAGCTCCAGCTCCCTCTTTTCTTCTATTCTTAGGGATCTATGTGTTCACTGTGGTGGGC
AACTTGGGCTTGATCACCTTAATTGGGATAAATCCTAGCCTTCACACCCCATGTACTTTT
CCTCTTCAACTTGTCTTTATAGATCTCTGTTATTCCTGTGTGTTACCCCAAAATGCTGA
ATGACTTTGTTTCAGAAAGTATCATCTCTTATGTGGGATGTATGACTCAGCTATTTTCTT
TGTTTCTTTGTCAATTCTGAGTGCTATGTGTTGGTATCAATGGCCTATGATCGCTATGTGGC
CATCTGCAACCCCTGCTCTACATGGTCACCATGTCCCAAGGGTCTGCTTTCTGCTGATGT
40 TTGGTTCCTATGTGGTAGGGTTTGCTGGGGCCATGGCCACACTGGAAGCATGCTGCGACT
GACCTTCTGTGATTCCAACGTCATTGACCATTATCTGTGTGACGTTCTCCCCCTCTTGCAGC
TCTCCTGCACCAGCACCCATGTGAGTGAGCTGGTATTTTTCATTGTTGTTGGAGTAATCACC
ATGCTATCCAGCATAAGCATCGTCATCTCTTACGCTTTGATACTCTCCAACATCCTCTGTAT
TCCTTCTGCAGAGGGCAGATCCAAAGCCTTAGCACATGGGGTCTCCACATAATTGCTGTT
GCTCTGTTTTTGGGTGAGGACATTACCTACTTAACAACATCTTTTCTGGCTCTATGAA
45 CCATGGCAGATTTGCCTCAGTCTTTACACCAATGTGGTTCCTGCTTAACCTTCGATCT
ACAGTTTGAGGAATAAGGATGATAAAGTGCCTGGGCAAAACCTGAAGAGAGTGCTCT
TCTAA (SEQ ID NO: 22)

AOLFR12 sequences:

50 MERNHNPDNCNVLNFFADKKNRRNFGQIVSDVGRICYSVLSLGEPTTMGRNNLTRPSEFIL
LGLSSRPEDQKPLFAVFLPIYLITVIGNLLILAIRSDTRLQTPMYFFLSILSFVDICYVTIIPKMLV
NFLSEKTIISYGECLTQMYFFLAFGNTDSYLLAAMADRYVAICNPFHYITIMSHRCCVLLVLS
FCIPHFHSLHILLTNQLFCASNVIHHFFCDDQPVLLKLSSSHVFKEITVMTEGLAVIMTFPSCIII
SYLRILITVLKIPSAAGKRKAFSTCGSHLTVVTLFYGSISYVYFQPLSNYTVKDQIATIIYTVLTP
55 MLNPFYISLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)

ATGGAAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTTCTTTGCTGATAAGA
 AGAATAAAAGGAGAAATTTTGGACAGATTGTATCAGATGTTGGAAGAATCTGTTACAGTG
 TTAGTTTATCTTTAGGTGAACCCACAACCTATGGGAAGAAATAACCTAACAGACCCCTCTGA
 ATTCATCCTCCTTGGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTCC
 5 TCCCCATCTACCTTATCACAGTGATAGGAAACCTGCTTATCATCCTGGCCATCCGCTCAGA
 CACTCGTCTCCAGACGCCCATGTACTTCTTTCTAAGCATCCTGTCTTTTGTGACATTGCT
 ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACCTTCTTATCAGAGACAAAGACCATCTC
 TTACGGTGAGTGTCTGACCCAGATGTACTTTTCTTAGCCTTTGGAAACACAGACAGTTAC
 CTGCTAGCAGCCATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA
 10 CCATTATGAGTCACAGATGCTGTGCTGCTTCTGGTTCTCTCCTTCTGCATTCCACATTTT
 CACTCCCTCCTGCACATTCTTCTGACTAATCAGCTCATCTTCTGTGCCTCCAATGTCATCCA
 TCACTTTTTCTGCGATGATCAACCAGTGCTAAAATTGTCCTGTTCTCCCATTTTGTCAAAG
 AAATCACAGTAATGACAGAAGGCTTGGCTGTGCTAATGACCCCGTTTTTCATGCATCATCAT
 CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCCTTCAGCTGCTGGAAAGCGTAAA
 15 GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCCTGTTTATGGAAGCATTAGCTA
 TGTCTATTTTACGCCCCCTGTCCAATACTGTCAAGGATCAAATAGCAACAATTATCTAC
 ACCGTAAGTACTCCTATGCTAAATCCATTTATCTATAGTCTGAGGAACAAAGACATGAAGC
 AGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

20 **AOLFR13 sequences:**

MDQKNGSSFTGFILLGFSDRPQLELVLFVLLIFYIFTLLGNKTIIVLSHLDPHLHNP MYFFFSNL
 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLSTECVLLGVMAFDRYAAVCRPL
 HYTVVMHPCLYVLMASWSWVIGFANSLLQTVLILLTLCGRNKLHFLCEVPPLLKLACVDTT
 MNESELFVSVIILLVPVALIIFSYSQIVRAVVRKISATGQRKVFGTCGSHLT VVSIFYGTAIYAY
 25 LQPGNNYSQDQGXISLFYTIITPMINPLIYTLRNKDVKGALKKVLWKYDSR (SEQ ID NO:
 25)

ATGGATCAGAAAAATGGAAGTTCTTTCACTGGATTATCCTACTGGGTTTCTCTGACAGGC
 CTCAGCTGGAGCTAGTCCTCTTTGTGGTTCTTTGATCTTCTATATCTTCACTTTGCTGGGG
 30 AACAAAACCATCATTGTATTATCTCACTTGGACCCACATCTTCACAATCCTATGTATTTTTT
 CTTCTCCAACCTAAGCTTTTTGGATCTGTGTTACACAACCGGCATTGTTCCACAGCTCCTGG
 TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTTCACTGTACAT
 CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT
 GCAGCTGTTTGCAGGCCCCCTCCACTACACAGTAGTCATGCACCCTTGTCTGTATGTGCTGA
 35 TGGCTTCTACTTCATGGGTCATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG
 CTTTAAACACTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCTCCATTGCT
 CAAGCTTGCCTGTGTTGACACTACTATGAATGAATCTGAACTCTTCTTTGTGAGTGTCTATTA
 TTCTTCTTGTACCTGTTGCATTAATCATATTCTCCTATAGTCAGATTGTCAGGGCAGTCGTG
 AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTTTGGGACATGTGGCTCCACCTCACA
 40 GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTTACCTCCAGCCCGGCAACAATACTC
 TCAGGATCAGGGCAAGKTCATCTCTCTTCTACACCATCATTACCCCATGATCAACCCC
 CTCATATATACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG
 AACTACGACTCCAGATGA (SEQ ID NO: 26)

45 **AOLFR14 sequences:**

MALPLLLSPSCFASSQSLSSRMNSENLTAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL
 LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYSYSAIGPKMLVDLLPRATIPYTACALQMF
 VFAGLADTECCLLAAMAYDRYVAIRNPLLYTTAMSQRLCLALLGASGLGGAVSAFVHTTLTF
 RLSFCRSRKINSFFCDIPPLLAISCSDSLNEILLFAICGFIQTATVLAITVSYGFIAGAVIHMRSVE
 50 GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALDTDKMASVFYTLVIPSLNPLIYSLRNKE
 VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG
 GATGAACTCAGAGAACCTCACCCGGGCGCGGTTGCCCTGCTGAATTCGTCTCCTGGGC
 55 ATCACAAATCGCTGGGACCTGCGTGTGGCCCTCTTCTGACCTGCCTGCCTGTCTACCTGG
 TGAGCCTGCTGGGAAACATGGGCATGGCGCTGCTGATCCGCATGGATGCCCGGCTCCACA

WO 01/98526

CACCTATGTACTTCTTCTGGCCAACTCTCCCTGCTGGATGCCTGCTATTCTCCGCCATC
 GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCCGAGCCACCATCCCTTACACAGCCTGTG
 CCCTCCAGATGTTTGTCTTTGCAGGTCTGGCTGATACTGAGTGTGCTTGGCAGCCAT
 5 GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATACAACAGCTATGTGCGAG
 CGTCTATGCCTGGCCTTGTGCTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCCTTTGTTC
 ACACAACCCTCACCTTCCGCCTGAGCTTCTGCCGCTCCCGGAAGATCAATGACTTCTTCTG
 CGATATCCCTCCACTGCTGGCCATCTCGTGACGTGACACCAGTCTCAATGAACTCCTTCTCT
 TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTAGCTATCACGGTGTCTTATGGCTT
 CATCGCTGGGGCTGTGATCCACATGCGCTCGGTGAGGGCAGTCGGCGAGCAGCCTCCAC
 10 CGGTGGTTCCACCTCACAGCCGTGGCCATGATGTACGGGACACTCATTTTCATGTACCTG
 CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCCTGG
 TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT
 CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGTCCAGTGA (SEQ ID NO: 28)

15 **AOLFR15 sequences:**
 MRENNQSSTLEFILLGVTGQQEQEDFFYILFLFIYPITLIGNLLIVLAICSDVRLHNP MYFLLANLS
 LVDIFFSSVTIPKMLANHLGSKSISFGGCLTQMYFMIALGNTDSYILAAMAYDRAVAISHPLH
 YTTIMSPRSCIWLIAGSWVIGNANALPHTLLTASLSFCGNQEVANFYCDITPLKLSCSDIHFHV
 KMMYLGVGIFSVPLLCIIVSYIRVFSTVQVPSTKGVLKAFSTCGSHLTVVSLYGTVMGTYFR
 20 PLTNYSLKDAVITVMTAVTPMLNPFYISLRNRMKAALRKLFNKRISS (SEQ ID NO: 29)

ATGAGGGAAAATAACCAGTCCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC
 AGGAACAGGAAGATTCTTCTACATCCTCTTCTGTTTACCTTACCCCATCACATTGATTGGA
 AACCTGCTCATTGTCCTAGCCATTTGCTCTGATGTTGCTTCAACCCCATGTATTTCT
 25 CCTTGCCAACTCTCCTTGGTTGACATCTTCTTCTCATCGGTAACCATCCCTAAGATGCTGG
 CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTGGGGGATGCCTAACGCAGATGTATTT
 CATGATAGCCTTGGGTAAACACAGACAGCTATATTTGGCTGCAATGGCATATGATCGAGCT
 GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTTGTATCTGGC
 TTATTGCTGGGTCTTGGGTGATTGGAAATGCCAATGCCCTCCCCACACTTGTCTCACAGC
 30 TAGTCTGTCTTCTGTGGCAACCAGGAAGTGGCCAACCTTCTACTGTGACATTACCCCTTG
 CTGAAGTTATCCTGTTCTGACATCCACTTTCATGTGAAGATGATGTACCTAGGGGTTGGCA
 TTTTCTCTGTGCCATTACTATGCATCATTGTCTCCTATATTGAGTCTTCTCCACAGTCTTCC
 AGGTTCTTCCACCAAGGGCGTGCTCAAGGCCTTCTCCACCTGTGGTTCCACCTCACGGT
 TGTCTCTTTGTATTATGGTACAGTCATGGGCACGTATTTCCGCCCTTTGACCAATTATAGCC
 35 TAAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTAAATCCTTTTCAT
 CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT
 CTCTCGTAA (SEQ ID NO: 30)

40 **AOLFR16 sequences:**
 MRRNCTLVTEFILLGLTSRRELQILLFTLFLAIYMTVAVGNLGMIVLIQANAWLHMP MYFFLSH
 LSFVDLCFSSNVTIPKMLEIFLSEKKSISYPAQLVQCYLFIALVHVEIYILAVMAFD RYMAICNPLL
 YGSRMSKSVCSFLITVPYVYGALTGLMETMWTYNLAFCGPNEINH FYCADPPLIKLACSDTYN
 KELSMFIVAGWNLSFSLFIICISYLYIFPAILKIRSTEGRQKAFSTCGSHLTA VTIFYATLFFMYLR
 PPSKESVEQGMVAVFYTTVIPMLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

45 ATGAGAAGAAACTGCACGTTGGTGACTGAGTTCATTCTCCTGGGACTGACCAGTCGCCGG
 GAATTACAAATTCTCCTCTTACGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA
 ACCTTGGCATGATTGTCCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTCT
 CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTTCCAATGTGACTCCAAAGATGCTGG
 50 AGATTTTCTTTTTCAGAGAAGAAAAGCATTTTCTATCCTGCCTGTCTTGTGAGTGTACCTT
 TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTTGACCGGTACAT
 GGCCATCTGCAACCCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGTGCTCCTTCTC
 ATCACGGTGCCTTATGTGTATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA
 ACCTAGCCTTCTGTGGCCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCTGAT
 55 TAAGCTGGCTTGTCTGACACCTACAACAAGAGTGTGCAATGTTTATTGTGGCTGGCTGG
 AACCTTTCTTTTCTCTTTCATCATATGATTTCCTACCTTACATTTTCCCTGCTATTTTA

AAGATTCGCTCTACAGAGGGCAGGCAAAAAGCTTTTTCTACCTGTGGCTCCCATCTGACAG
CTGTCACTATATTCTATGCAACCCTTTTCTTCATGTATCTCAGACCCCCCTCAAAGGAATCT
GTTGAACAGGGTAAAAATGGTAGCTGTATTTTATACCACAGTAATCCCTATGCTGAACCTTA
TAATTTATAGCCITAGAAAATAAAAATGTAAAAAGAAGCATTAAATCAAAGAGCTGTCAATGA
5 AGATATACTTTTCTTAA (SEQ ID NO: 32)

AOLFR17 sequences:

MLNFTDVTEFILLGLTSRREWQVLFHIFLVVYIITMVGNIGMMVLIKVSPQLNNPMYFFLSHLS
FVDVWFSSNVTPKMLENLFSDKKTITYAGCLVQCFFIALVHVEIFILAAMAFDRYMAIGNPLL
10 YGSKMSRVVCIRLITFPYIYGFLTSLAATLWTYGLYFCGKIEINHFCADPPLIKMACAGTFVKE
YTMILLAGINFTYSLTVIISYLFILAILRMRSAGEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE
ESVEQGKMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGAGAAT
15 GGCAAGTTCTCTTCTTCATCATCTTTCTTGTGGTCTACATCATCACCATGGTGGGCAATATC
GGCATGATGGTGTTAATCAAGGTCAGTCCTCAGCTTAACAACCCCATGTACTTTTTCTCA
GTCACCTTGTCATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAC
CTGTTTTTCAGATAAAAAACAATTACTTATGCTGGTGTGTTAGTACAGTGTCTTCTTCTCAT
TGCTCTTGTCCATGTGGAAATTTTATTCTTGTGCGATGGCCTTTGATAGATACATGGCAA
20 TTGGGAATCCTCTGCTTATGGCAGTAAAATGTCAAGGGTGTCTGTATTGACTGATTAC
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT
ACTTCTGTGAAAAAATTGAGATCAACCATTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGATCATACTTGCCGGCATTAACCTC
ACATATTCCCTGACTGTAATTATCATCTCTTACTTATTATCATCCTCATTGCCATTCTGCGAAT
25 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 34)

30

AOLFR18 sequences:

MSNTNGSAITEFILLGLTDCPELQSLFLVFLVVYLVTLLGNLGMIMLMRLDSRLHTPMYFFLT
NLA FVDLCYTSNATPQMSNIVSEKTISFAGCFTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP
LRYSVKTSRRVCICLATFPYVYGFSDGLFQAILTFRLTFCRSNVINHFYCADPPLIKLSCSDTYVK
35 EHAMFISAGFNLSSSLTTVLVSYAFILAILRIKSAEGRHKAFSTCGSHMMAVTLFYGTLFCMYI
RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDVKQALKNVLR (SEQ ID NO: 35)

ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC
CGGAACTCCAGTCTCTGCTTTTTGTGCTGTTTCTGGTTGTTTACCTCGTCACCCTGCTAGGC
40 AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTCACACGCCCATGTACTTCT
TCCTCACTAACTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC
GACTAATATCGTATCTGAGAAGACCATTTCTTTGCTGGTGTCTTTACACAGTGCTACATTT
TCATTGCCCTTCTACTCACTGAGTTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT
GGCCATATATGACCCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTTTGCATCTGCTTG
45 GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCCATCCTGACCTTCCG
CCTGACCTTCTGTAGATCCAATGTCATCAACCACTTCTACTGTGCTGACCCGCCGCTCATT
AGCTTTCTTGTCTGATACTTATGTCAAAGAGCATGCCATGTTTCATATCTGCTGGCTTCAAC
CTCTCCAGCTCCCTCACCATCGTCTTGGTGTCTATGCCTTCATTCTTGCTGCCATCCTCCG
GATCAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCTCATATGATGGC
50 TGTCACCCTGTTTTATGGGACTCTTTTTGCATGTATATAAGACCACCAACAGATAAGACT
GTTGAGGAATCTAAAATAATAGCTGTCTTTTACACCTTTGTGAGTCCGGTACTTAATCCAT
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCCTGAGATGA
(SEQ ID NO: 36)

55

AOLFR19 sequences:

METKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLTAVGNVLIILAIYSDPRLHTPMYFFLSNL
 SFMDICFTTVIVPKMLVNFLSETKIISYVVGCLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH
 YDVVMKPWHCLLMLLGSCSISHLHLFRVLLMSRSLFCASHIHKHFFCDTQPVLKLSGSDTSSSQ
 5 MVVMTETLA VIVTPFLCTIFSYLQIIVTVLRIPSAAGKWKAFTSCGSHLTVVLFYGSVIYVYFR
 PLSMYSVMKGRVATVMYTVVTPMLNPFYSLRNKDMKRGLKLRHRIYS (SEQ ID NO: 37)

 ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCA
 ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCCTCATCATGTACCTACTCACTGCGGTG
 10 GGGAAATGTGCTCATCCTGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACT
 TTTTCTCAGCAACTTGTCTTTCATGGATATCTGCTTCACAACAGTCATAGTGCCTAAGATG
 CTGGTGAATTTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT
 ACTTCTTCATGGCATTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG
 GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA
 15 CTCATGCTATTGGGTCTTGCAGCATCTCCCACCTACATTCCCTGTTCCGCGTGCTACTTAT
 GTCTCGCTTGTCTTCTGTGCCTCTCACATCATTAAGCACTTTTCTGTGACACCCAGCCTG
 TGCTAAAGCTCTCCTGCTCTGACACATCTCCAGCCAGATGGTGGTGATGACTGAGACCTT
 AGCTGTCAATTGTGACCCCTTCTGTGTACCATCTTCTCCTACCTGCAAATCATCGTCACTG
 TGCTCAGAATCCCCTCTGCAGCCGGGAAGTGAAGGCCTTCTTACCTGTGGCTCCCACCT
 20 CACTGTAGTGGTCTGTCTATGGGAGTGTCTATGTCTATTTAGGCCTGTGTCATGT
 ACTCAGTGATGAAGGGCCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGTCTGA
 ACCCTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTGAAGAAATTAAGAC
 ACAGAATTTACTCATAG (SEQ ID NO: 38)

AOLFR20 sequences:

25 MVEENHTMKNEFILTGFTHPELKTLLFVVFVFAIYLITVVGNSLVALIFTHCRLHTPMYIFLGN
 LALVDSGCCAATPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLAAVAYDRYVAICNP
 LQYHIMMSKKLCIQMTTGAFIAGNLHSMIHVGLVFRLVFCGLNHNHFYCDTLPYRLSCVDPF
 INELVLFIFSGSVQVFTIGSVLISYLYILLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFLYIRP
 30 NLLEEGNDIPAAILFTIVVPLNPFYSLRNKEVISVLRKILLIKISQGSVNK (SEQ ID NO: 39)

ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCCTCACAGGATTTACAGATCACC
 CTGAGCTGAAGACTCTGCTGTTTGTGGTGTCTTTGCCATCTATCTGATCACCCTGGTGGG
 GAATATTAGTTTGGTGGCACTGATATTTACACACTGTGCGCTTCACACACCAATGTACATC
 35 TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGTCTGTGCCTGTGCTATTACCCCCAAAATGTT
 AGAGAACTTCTTTCTGAGGGCAAAGGATTTCCCTCTATGAATGTGCAGTACAGTTTTAT
 TTTCTTGTCACTGTGAAACTGCAGACTGCTTTCTTCTGGCAGCAGTGGCCTATGACCGCT
 ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAACTCTGCATTCA
 GATGACCACAGGCGCTTCATAGCTGGAAATCTGCATTCCATGATTCTGTAGGGCTTGTA
 40 TTTAGGTTAGTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT
 GTATAGACTCTCCTGTGTTGACCCTTTCATCAATGAACCTGTTCTATTCTCTTACTATT
 CAGTTCAAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATTCTTCTTACTATT
 TTCAGAATGAAATCCAAGGAGGGAAGGGCCAAAGCCTTTTCTACTGTGCATCCCACTTTT
 CATCAGTTTCATTATTCTATGGATCTATTTTCTTATACATAGTAGTTCCCTTACTAAATC
 45 GAAGGAGGTAATGATATACCAGCTGCTATTTTCTTATACATAGTAGTTCCCTTACTAAATC
 CTTTCATTTATAGTCTGAGAAACAAGGAAGTAATAAGTGTCTTAAGAAAAATTCTGCTGAA
 AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

AOLFR21 sequences:

50 MEPRKNVTDVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVTVTVSETLGSPMSFFLAGL
 TFIDIIYSSSISRLISDLFFGNNSISFQSFMAQLFIEHLFGGSEVFLLLVMAYDRYVAICKPLHYLV
 IMRQWVCVLLLVSWVGGFLQSVFQLSIHYGLPFCGPNVIDHFFCDMYPLLKLACTDTHVIGLL
 VVANGGLSCTIAFLLLISYGVILHSLKKLSQKGRQKAHSTCSSHITVVVFFVPCIFMCARPAR
 TFSIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)

TCACCCTCTCCTTCTGTAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCCACCCCTG
 CTGAAGCTTGCCTGCAGTGACACAGCAAACATCGAGATTGTATCATCTTCTTTGGCAATT
 TTGTGATTTTGGCCAATGCCTCCGTCATCCTGATTTCTATCTGCTCATCATCAAGACCATT
 TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCCTCTCACATCA
 5 CTGCTGTGGCCCTTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAAA
 TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCATGCTGAACC
 CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAAGACGCCTTCAGAAAGGTCGCTAGGA
 GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

10 **AOLFR25 sequences:**

METGNLTWVSDFVFLGLSQTRELQRFLFLMFLFVYITTVMGNILIIITVTSDSLHTPMYFLLRN
 LAVLDLCFSSVTAPKMLVDLLSEKKTISYQCGMGQIFFHFLGGAMVFFLSVMAFDRLIAISRPL
 RYVTVMNTQLWVGLVVA TWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVLR LACTDT
 SLLEFLKISNSGLLDVWVFFLLMSYLFILVMLRSHPGARRKAASTCTTHIVVSMIFVPSIYLY
 15 ARPFTPFMDKLV SIGHTVMT PMLNPMIYTLRNQDMQAAVRRLGRHRLV (SEQ ID NO: 47)

ATGGAAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCTGTTGGGCTCTCGCAGACTC
 GGGAGCTCCAGCGTTTCTGTTTCTAATGTTCTGTTTGTCTACATCACCCTGTTATGGGA
 AACATCCTTATCATCATCACAGTGACCTCTGATCCAGCTCCACACACCCATGTACTTTCT
 20 GCTCCGAAACCTGGCTGTCTAGACCTCTGTTTCTTTCAGTCACTGCTCCCAAAATGCTAG
 TGGACCTCCTCTCTGAGAAGAAAACCATCTCTTACCAGGGCTGCATGGGTGAGATCTTCTT
 CTTCCACTTTTTGGGAGGTGCCATGGTCTTCTTCTCTCAGTGATGGCCTTTGACCGCTCA
 TTGCCATCTCCCGGCCCTCCGCTATGTACCGTCATGAACACTCAGCTCTGGGTGGGGCT
 GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC
 25 CCACTGCCCTTCTGTGGCCCCAACATTTTGATAACTTCTACTGTGATGTTCCCCAAGTACT
 GAGACTTGCCTGCACTGACACCTCACTGCTGGAGTTCTCAAGATCTCCAACAGTGGGCTG
 CTGGATGTCGTCTGGTTCTTCTCCTCCTGATGTCTACTTATTATCCTGGTGTGCTGAG
 GTCACATCCAGGGGAGGCAAGAAGGAAGGCAGCTTCCACCTGCACCAACCCACATCATCGT
 GGTTTCCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCGGCCCTTCACTCCATTCCCTA
 30 TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCATGCTCAACCCCATGATCTA
 TACCTGAGGAACCAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT
 TTGA (SEQ ID NO: 48)

AOLFR26 sequences:

35 MAAKNSSVTEFILEGLTHQPGLRIPLFFLFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLFNLS
 LIDFCFSTTITPKMLMSFVSRKNHSFTGCMTQLFFFCFFVSESFILSAMAYDRYVAICNPLLYT
 VTMSCQVCLLLLLGAYGMGFAGAMAHTGSIMNLTFCADNLVNHFMCIDLPLELSCNSSYMN
 ELVVFIVVAVDVGMPIVTVFISYALILSSILHNSSTEGRSKAFSTCSSHIIVVSLFFGSGAFMYLKP
 LSILPLEQGVSSLFYTHIVPVLNPLIYSLRNKDVKVALRRTLGRKIFS (SEQ ID NO: 49)

40 ATGGCAGCCAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG
 GACTGCGGATCCCCCTCTTCTTCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAA
 CCTGGGCTTGATAACCCTGATTGGGCTGAACCTCTCACCTGCACACTCCCATGTACTTCTTCC
 TTTTAAACCTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAAATGCTGATG
 45 AGTTTGTCTCAAGGAAGAACATCATTTCTTTCACAGGGTGTATGACTCAGCTCTTCTTCTT
 CTGCTTCTTTGTCTGTCTGAGTCCTTCATCCTGTGAGCGATGGCGTATGACCGCTACGTGG
 CCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTGCTCCTTTTG
 TTGGGTGCCTATGGGATGGGGTTTGTGGGGCCATGGCCACACAGGAAGCATAATGAAC
 CTGACCTTCTGTGCTGACAACCTTGTCATCATTTTCATGTGTGACATCCTTCTCCTTGA
 50 GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTGGTGGCTGTGAC
 GTTGGAAATGCCCATGTCACTGTCTTTATTTCTTATGCCCTCATCCTCTCCAGCATTCTACA
 CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAAGTCCACATAATTGTA
 GTTTCTCTTTTCTTTGGTTCTGGTGTCTTTCATGTATCTCAAACCCCTTTCCATCCTGCCCTC
 GAGCAAGGGAAAGTGTCTCCTGTTCTATACCATAATAGTCCCCGTGTTAAACCCATTAA
 55 TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAA
 TCTTTTCTTAA (SEQ ID NO: 50)

AOLFR27 sequences:

- MPSQNYSIIEFNLFQFSAFPQHLLPILFLLYLLMFLFTLLGNLLIMATIWIHRLHTPMYFLCTL
 SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR
 5 YNVLMSPRDCAHLVACTWAGGSVMGMMVTTIVFHLTFCGSNVIHHFFCHVLSLLKLACENKT
 SSVIMGVMLVCVTALIGCLFLIILSYVFIVAAILRIPSAEGRHKTFTSTCVSHLTVVTVTHYSFASFIY
 LKPKGLHSMYSDALMATTYTVTFPFLSPIIFSLRNKELKNAINKNFYRKFCPPSS (SEQ ID NO:
 51)
- 10 ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTTCCC
 CCAGCACCTCCTGCCCATCTTGTTCTGCTGTACCTCCTGATGTTCTGTTACATTGCTGG
 GCAACCTTCTCATGCGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT
 CTCTTGTCACCCCTCTCCGTCTCTGAGATTCTGTTCACTGTTGCCATCACCCCTCGCATGC
 TGGCTGATCTGCTTTCCACCCATCATTCCATCACCTTTGTGGCTTGTGCCAACCATGTTT
 15 TTCTCTTCATGTTTGGCTTCACTCACTCCTTCTCTCTGCTCATGGGCTATGATCGCTA
 TGTGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCGTGACTGTGCCCAT
 CTTGTGGCCTGTACCTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAACGATAGTTT
 TCCACCTCACTTTCTGTGGGTCTAATGTGATCCACCATTCTTCTGTCTGCTTTCCCTCT
 TGAAGTTGGCCTGTGAAAACAAGACATCATCTGTCTCATGTTGTTGCTTCTGTTGCTGCT
 20 CACAGCCCTGATAGGCTGTTTATTCTCATCATCTCTCTCTATGTCTTCACTGTGGCTGCCA
 TCTTGAGGATTCCCTCTGCCGAAGGCCGACACAGACATTTTCTACGTGTGTATCCACCT
 CACTGTGGTGGTCACGCACTATAGTTTGCCTCTTTATCTACCTCAAGCCCAAGGGCTCC
 ATTCTATGTACAGTGACGCTTGATGGCCACCACCTATACTGTCTTACCCCTTCTTACG
 CCAATCATTTTACGCTAAGGAACAAGGAGCTGAAGAATGCCATAAATAAAAACTTTTACA
 25 GAAAATTCTGTCTCCAAGTTCCTGA (SEQ ID NO: 52)

AOLFR28 sequences:

- MPNFTDVTEFTLLGLTCRQELQVLFVFLAVYMITLLGNIGMIILISISPQLQSPMYFFLSHLSE
 ADVCFSSNVTPKMLENLLSETKTISYVGCLVQCYFFIAVVHVEVYILAVMAFDRYMAGCXPLL
 30 YGSKMSRSTVCVRLISVXYXYGFSVSLICLWYGLYFCGNFEINHIFYCADPPLIQIACGRVHIKE
 ITMIVIAGINFTYSLSVLISYTLIVVAVLRMRADGRRKAFSTCGSHLTAVSMFYGTPIFMYLR
 RPTESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKEAVNKAITKTYVRQ (SEQ ID NO: 53)
- 35 ATGCCTAATTTACGGATGTGACAGAATTTACTCTCCTGGGGCTGACCTGTGCTCAGGAGC
 TACAGGTTCTCTTTTTGTGGTGTTCCTAGCGTTTACATGATCACTCTGTTGGGAAATATT
 GGTATGATCATTTTGATTAGCATCAGTCCTCAGCTTCAGAGTCCCATGTACTTTTCTGAG
 TCATCTGTCTTTTGGGACGTGTGCTTCTCCTCCAACGTTACCCCCAAATGCTGGAAAAT
 TATTATCAGAGACAAAAACCATTTCTATGTGGGATGCTTGGTGACGTGCTACTTTTCAT
 TGCCGTTGTCCACGTGGAGGTCTATATCCTGGCTGTGATGGCCTTTGACAGGTACATGGCC
 40 GGCTGCAANCCTCTGCTTTATGGCAGTAAATGTCTAGGACTGTGTGTGTTTCGGCTCATCT
 CTGTGNNTATGNNTATGGATTCTCTGTGACGCTAATATGCACACTATGGACTTATGGCTT
 ATACTTCTGTGGAACTTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCTCATCCAGA
 TTGCCTGTGGGAGAGTGCACATCAAAGAAATCACAATGATTGTTATTGCTGGAATTAACCT
 CACATATCCCTCTCGGTGGTCTCTCTCTACACTCTCATTGTAGTGTGCTACGCA
 45 TGCGCTCTGCCGATGGCAGGAGGAAGGCGTTCTCCACCTGTGGGTCCCACTTGACGGCTGT
 TTCTATGTTTTATGGACCCCCATCTTCATGTATCTCAGGAGACCCACTGAGGAATCCGTA
 GAGCAGGGCAAAATGGTGGCTGTGTTTTACACCACAGTAATTCCTATGTTGAATCCCATGA
 TCTACAGTCTGAGAAATAAGGATGTAAAAGAAGCAGTCAACAAAGCAATCACCAAGACAT
 ATGTGAGGCAGTAA (SEQ ID NO: 54)
- 50

AOLFR29 sequences:

- MMSFAPNASHSPVFLLLGFSRANISYTLFFLFLAIYLTTLGNVTLVLLISWDSRLHSPMYLLR
 GLSVIDMGLSTVTLPLLAHLVSHYPTIPAARCLAQFFFFYAFGVTDTLVIAVMALDRYVAICD
 PLHYALVMNHQRCACLLALSWSILHTMLRVGLVPLCWTGDAGGNVNLPHFFCDHRPLLR
 55 ASCSDIHSNELAIFEGGFLMLGPCALIVLSYVRIGAAILRLPSAAGRRRAVSTCGSHLTMVGFL

TCCTCTGCCATTTGGCCTTTGTAGACATTGGGTACTCCTCATCAGTCACACCTGTCATGCTC
 ATGAGCTTCCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCAGCTCTGTT
 CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCCTGCTGGCTGCCATGGCCTATGATCGCTA
 TGTGGCCATCTGCTCACCCCTGCTCTACTCTACCTGCATGTCCCTGGAGTCTGCATCATCT
 5 TAGTGGGCATGTCTACCTGGGTGGATGTGTGAATGCTTGGACATTCAATTGGCTGCTTATT
 AAGACTGTCCTTCTGTGGGCCAAATAAAGTCAATCACTTTTTCTGTGACTATTCACTCTT
 TGAAGCTTGCTTGTCCCATGATTTTACTTTTGAAATAATTCCAGCTATCTCTTCTGGATCT
 ATCATTGTGGCCACTGTGTGTGTCATAGCCATATCCTACATCTATATCCTCATCACCATCCT
 GAAGATGCACTCCACCAAGGGCCGCCACAAGGCCTTCTCCACCTGCACCTCCCACCTCACT
 10 GCAGTCACTCTGTTCTATGGGACCATTACCTTCATTTATGTGATGCCCAAGTCCAGCTACTC
 AACTGACCAGAACAAAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCCCATGTTGAACCCC
 CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA
 AAAATATTTTCTTGA (SEQ ID NO: 60)

15 **AOLFR32 sequences:**

MNSLKDGNHTALTGFILLGLTDDPILRVILFMIILSGNLSIIILIRISSQLHHPMYFFLSHLAFADM
 AYSSSVTPNMLVNFLVERNVSYLGCALQLSAAFFATVECVLLAAMAYDRFVAICSPLLYSTK
 MSTQVSVQLLL VVYIAGFLIAVSYTTSFYLLFCGPNQVNHFFCDFAPLLELSCSDISVSTVLSF
 SSGSIIVTVCVIAVCYIYILITILKMRSTEGHHKAFSTCTSHLT VVTLFYGTITFIYVMPNFSYST
 20 DQNKVSVLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNDIT (SEQ ID
 NO: 61)

ATGAATTCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA
 CAGATGATCCAATCCTTCGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA
 25 ATTATTCTTATCAGAATTCTTCTCAGCTCCATCATCCTATGTATTTCTTTCTGAGCCACTT
 GGCTTTTGCTGACATGGCCTATTTCATCTTCTGTACACCCCAACATGCTTGAAACTTCCTGG
 TGGAGAGAAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTCAGCGGCTTTCTT
 TGCAACAGTCGAATGCGTCCTTCTGGCTGCCATGGCCTATGACCGCTTTGTGGCAATTTGC
 AGTCCACTGCTTTATTCAACCAAAAATGTCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG
 30 TTTACATAGCTGGTTTTCTCATTGCTGTCTCCTATACTACTTCTCTTCTATTTTTTACTCTTCT
 GTGGACCAATCAAGTCAATCAATTTTTCTGTGATTTGCTCCCTTACTTGAACCTCTCCTGT
 TCTGATATCAGTGTCTCCACAGTTGTTCTCTCATTCTTCTGGATCCATCATTGTGGTCAC
 TGTGTGTGTCATAGCCGTCTGCTACATCTATATCCTCATCACCATCCTGAAGATGCGCTCCA
 CTGAGGGGACCAACAAGGCCTTCTCCACCTGCACCTCCCACCTCACTGTGGTTACCTGTT
 35 CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTTAGCTACTCAACTGACCAGAAC
 AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC
 TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTTAGAAAAATACTTTCTC
 ATGATGCTTGTTATTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

40 **AOLFR34 sequences:**

MLEGVEHLLLLLLLDVNSKELQSGNQTSVSHFILVGLHHPQLGAPLFLAFLVITYLLTVSGNG
 LIILTVLVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRIISFGGCVIQLFSFHLGCT
 ECFLYTLMA YDRFLAICKPLHYATIMTHRVCNSLALGTWLGGTIHSFQTSFVFRLPFCGPNRV
 DYIFCDIPAMRLACADTA INELVTFADIGFLALTCFMLILTSYGYIVAAILRIPSADGRRNAFST
 45 CAAHLTVVIVYYVPCTFIYLRPCSQEPLDGVVAVFYTVITPLLNSIHYTLCKEMKAALQRLGG
 HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG
 AACTGCAAAGTGGAACCAAGACTTCTGTGTCTCACTTCATTTTGGTGGGCCTGCACCACCC
 50 ACCACAGCTGGGAGCGCCACTCTTCTTAGCTTTCCTTGTCTATCTCCTCACTGTTTCTG
 GAAATGGGCTCATCATCCTCACTGTCTTAGTGGACATCCGGCTCCATCGTCCCATGTGCTT
 GTTCTGTGTACCTCTCCTTCTTGGACATGACCATTTCTTGTGCTATTGTCCCAAGATGC
 TGGCTGGCTTTCTTGGGTAGTAGGATTATCTCCTTTGGGGGCTGTGTAATCCAACATTTT
 TCTTTCCATTTCTGGGCTGTACTGAGTGCTTCTTTACACACTCATGGCTTATGACCGTTT
 55 CTTTGCCATTTGTAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCCC
 TGGCTTAGGCACCTGGCTGGGAGGGACTATCCATTCACTTTTCCAAACAAGTTTTGTATT

WO 01/98526

5 CCGGCTGCCCTTCTGTGGCCCCAATCGGGTCGACTACATCTTCTGTGACATTCCTGCCATGC
 TCGCTCTAGCCTGCGCCGATACGGCCATCAACGAGCTGGTCACCTTTGCAGACATTGGCTT
 CCTGGCCCTCACCTGCTTCATGCTCATCTCACTTCTATGGCTATATTGTAGCTGCCATCC
 TGCGAATTCGTCAGCAGATGGGCGCCGAATGCCTTCTCCACTTGTGCTGCCACCTCAC
 TGTGTGCTATTGTTTACTATGTGCCCTGCACCTTCATTTACCTGCGGCCTTGTTCACAGGAGC
 CCCTGGATGGGGTGGTAGCTGTCTTTTACACTGTACACTCCCTTGTCTAACTCCATCATC
 TACACACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGGCCACAAGGAA
 GTGCAGCCTCACTGA (SEQ ID NO: 64)

10 **AOLFR35 sequences:**
 MEPLNRTEVSEFFLKGFSGYPALHLLFPLCSAMYLVTLGNTAIMAVSVLDIHLHTPVYFFLG
 NLSTLDICYTPTFVPLMLVHLLSSRKTFISFVCAIQMCLSLSTGSTECLLAITAYDRYLAICPL
 RYHVLMSHRLCVLLMGAAWVLCCLKSVTEMVISMRLPFCGHHVVSHTCKILAVLKLACGNT
 SVSEDFLLAGSILLPVPLAFICLSYLLILATILRVPSAARCCAFSTCLAHLAVVLLFYGTIIFMY
 15 LKPKSKEAHISDEVFTVLYAMVTTMLNPTIYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO:
 65)

20 ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTCTTTTCTGAAAGGATTTTCTGGCTACC
 CAGCCCTGGAGCATCTGCTCTTCCCTCTGTGCTCAGCCATGTACCTGGTGACCTCCTGGG
 GAACACAGCCATCATGGCGGTGAGCGTGCTAGATATCCACCTGCACACGCCGTGTACTTC
 TTCCTGGGCAACCTCTCTACCCTGGACATCTGCTACACGCCACCTTTGTGCCTCTGATGCT
 GGTCCACCTCCTGTATCCCGGAAGACCATCTCCTTTGCTGTCTGTGCCATCCAGATGTGTC
 TGAGCCTGTCCACGGGCTCCACGGAGTGCTGCTACTGGCCATCACGGCCTATGACCGCTA
 CCTGGCCATCTGCCAGCCACTCAGGTACCAGTGCTCATGAGCCACGGGCTCTGCGTGCTG
 25 CTGATGGGAGCTGCCTGGGTCTCTGCCTCCTCAAGTCGGTGACTGAGATGGTCATCTCCA
 TGAGGCTGCCCTTCTGTGGCCACCAGTGGTCAGTCACTTCACCTGCAAGATCCTGGCAGT
 GCTGAAGCTGGCATGCGGCAACACGTCGGTCAGCGAAGACTTCTGCTGCGGGCTCCAT
 CCTGCTGCTGCCTGTACCCCTGGCATTATCTGCCTGTCTACTTGTCTATCCTGGCCACCA
 TCCTGAGGGGTGCCCTCGGCCGCCAGGTGCTGCAAGCCTTCTCCACCTGCTTGGCACACCT
 30 GGCTGTAGTGTCTTTTCTACGGCACCATCATCTTCATGTACTTGAAGCCCAAGAGTAAG
 GAAGCCACATCTCTGATGAGGTCTTCACAGTCCTCTATGCCATGGTCACGACCATGCTGA
 ACCCCACCATCTACAGCCTGAGGAACAAGAGGTGAAGGAGGCCAGGAAGGTGTGGG
 GCAGGAGTCGGGCCTCCAGGTGA (SEQ ID NO: 66)

35 **AOLFR36 sequences:**
 MYLVTVLRNLLSILAVSSDSHPHTPMYFFLSNLCWADIGFTLATVPKMIVDMGSHSKVISYGG
 CLTQMSFLVLFACIVDMFLTVMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFLSLLDSQLHS
 WIVLQFTFFKNVEISNFVCEPSQLKLASYDSVINSIFIYDNTMFGFLPISGILLSYKIVPSILRIS
 SSDGKYKAFAACGCHLAVVCLFYGTGIGVYLSAVAPPLRNGMVASVMYAVVTPMLNPFYIS
 40 LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKGQPHSIPTSANPAP (SEQ ID NO: 67)

45 ATGTATCTGGTCACGGTGCTGAGGAACCTGCTCAGCATCCTGGCTGTGAGCTCTGACTCCC
 ACCCCACACACCCATGTACTTCTCCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
 TTGGCCACGGTTCCCAAAATGATTGTGGACATGGGGTCGCATAGCAAAGTCATCTCTTATG
 GGGGCTGCCTGACACAGATGTCTTTCTTGGTACTTTTGCATGTATAGTAGACATGTTCTT
 GACTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTGCGCCCTCTGCACTACCCAGTCATC
 GTGAATCCTCACCTCTGTGTCTTCTCGTTTTGGTGTCCTTTTCTTACCTGTTGGATTCC
 CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTCAAGAATGTGGAAATCTCTAATT
 TTGTCTGTGAGCCATCTCAACTTCTCAAGCTTGCCCTTATGACAGCGTCATCAATAGCATA
 50 TATATAATTTGATAATACTATGTTTGGTTTTCTTCCCATTTACAGGATCCTTTTGTCTTAC
 CAGCCTGTGGCTGTACCTGGCAGTTGTTTGTCTTATTTATGGAACAGGCATTGGCGTGTA
 CCTGACTTCAGCTGTGGCACCACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTACGCT
 GTGGTCACCCCATGCTGAACCCCTTTCATCTACAGCCTGAGAAACAGGGACATTCAAAGTG
 55 CCCTGTGGAGGGTGTGCAACAAAACAGTCGAATCTCATGATCTGTTCCATCCTTTTCTTG

TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCCCTTAG
(SEQ ID NO: 68)

AOLFR37 sequences:

5 MEKANETSPVMGFVLLRLSAHPELEKTFVLLMYLVILLGNGVLILVTILDSRLHTPMYFFLG
NLSFLDICFTTSSVPLVLDSTLTPQETISFSACAVQMALSFAMAGTECLLSMMAFDYVAICNP
LRYSVIMSKAA YMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS
INVISMEVTNVIFLGVPVLFISFSYVFIITILRIPSAEGRKKVFSTCSAHLTVVIVFYGTLFFMYG
KPKSKDSMGADKEDLSDKLIPLFYGVVTPMLNPIHYSRLNKDVKA AVRLLRPKGFTQ (SEQ ID
10 NO: 69)

ATGGAAAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACCTCGTGATCCTGCT
GGGCAATGGGGTCCCTCATCCTGGTGACCATCCTTGACTCCCGCCTGCACACGCCCATGTAC
15 TTCTTCCTAGGGAACCTCTCCTTCCTGGACATCTGCTTCACTACCTCCTCAGTCCCCTGGT
CCTGGACAGCTTTTTGACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG
GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGTATC
GCTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT
GCCCATGGCTGCCAGCTCCTGGGCTATTGGTGGTGCTGCTTCCGTGGTACACACATCCTTG
20 GCAATTCAGCTGCCCTTCTGTGGAGACAATGTCATCAACCACTTCACCTGTGAGATTCTGG
CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA
TGTGATCTTCCTAGGAGTCCCGGTTCTGTTTCATCTCTTCTCCTATGTCTTCATCATACCA
CCATCCTGAGGATCCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCA
CCTCACCGTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTTAAGTCT
25 AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAAACTCATCCCCCTTTCTATG
GGGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG
CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

AOLFR38 sequences:

30 MYLVTVLRNLLIILAVSSDHLHTPMCFFLSNLCWADIGFTSAMVPKMIVDMQSHSRVISYAGC
LTQMSFFVLFACIEDMLLTVMAYDRFVAICHPLHYPVIMNPHLGVLVLVSFFLSLLDSQLHSW
IVLQFTFFKNVEISNFVCDPSQLNLACSDSVINSIFTYLD SIMFGFLPISGILLSYANNVPSILRISS
SDRKSKAFTSCGSHLAVVCLFYGTGIGVYLTS AVSPPRNGVVASV MYAVVTPMLNPFYSLR
NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)

35 ATGTACCTGGTCACGGTGCTGAGGAACCTGCTCATCATCCTGGCTGTCAGCTCTGACTCCC
ACCTCCACACCCCCATGTGCTTCTCCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
TCGGCCATGGTTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTCTTATG
CGGGCTGCCTGACACAGATGTCTTTCTTTGTCTTTTTCATGTATAGAAGACATGCTCCTG
40 ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTCAACCCCTGCACTACCCAGTCATCA
TGAATCCTCACCTTGGTGCTTCTTAGTTTTGGTGCTTTTTCTCAGCCTGTTGGATTCC
CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTCAAGAATGTGGAAATCTCCAATT
TTGTCTGTGACCCATCTCAACTTCTCAACCTTGCCTGTTCTGACAGTGTCATCAATAGCATA
TTCATATAITTAGATAGTATTATGTTTGGTTTTCTTCCCATTTCAGGGATCCTTTTGTCTTAC
45 GCTAACAATGTCCCCTCCATTCTAAGAATTCATCATCAGATAGGAAGTCTAAAGCCTTCT
CCACCTGTGGCTCTCACCTGGCAGTTGTTTGTCTATTTTATGGAACAGGCATTGGCGTGTA
CCTGACTTCAGCTGTGTCAACACCCCCCAGGAATGGTGTGGTGGCATCAGTGATGTACGCT
GTGGTCAACCCCATGCTGAACCCTTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG
CCCTGTGGAGGCTGCGCAGCAGAACAGTGAATCTCATGATCTGTTATCTCAAGATCTGCT
50 CCATCCTTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

AOLFR39 sequences:

MGVKNHSTVTEFLSLGLEQAELQLPLFLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS
LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFFCVVCVISECYMLAAMACDRYVAICSPL
55 LYRVIMSPRVCSLLVA AVFSVGFTDAVIHGGCILRLSFCGSNIUKHYFCDIVPLIKLSCSSTYIDEL

5 ATGGGTGTAAAAAACCATTCACAGTGACTGAGTTTCTTCTTTTCAGGATTAACCTGAACAAG
CAGAGCTTCAGCTGCCCCTCTTCTGCCTCTTCTTAGGAATTACACAGTTACTGTGGTGGG
AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCCATGTACTAT
TTCCTGAGTAGTTTGTCTTTTTTAGATTTCTGCTATTCTTCTGTCAATACCCCTAAAATGCT
ATCAGGGTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTCAGCTGTTTT
TTTTCTGTGTTTGTGTTATTTCTGAATGCTACATGCTGGCAGCCATGGCCTGCGATCGCTAC
10 GTGGCCATCTGCAGCCCACTGCTCTACAGGGTCATCATGTCCCCTAGGGTCTGTTCTCTGC
TGGTGGCTGCTGTCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTTGTATACT
CAGGTTGTCTTTCTGTGGATCAAACATCATTAAACATTATTTCTGTGACATTGTCCCTCTTA
TTAAACTCTCCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTTGTCATTGGTGGATTT
AACATGGTGGCCACAAGCCTAACAAATCATTATTTTCATATGCTTTTATCCTCACCAGCATCCT
15 GCGCATCCACTCTAAAAAGGGCAGGTGCAAAGCGTTTAGCACCTGTAGCTCCACCTGACA
GCTGTTCTTATGTTTTATGGGTCTCTGATGTCCATGTATCTCAAACCTGCTTCTAGCAGTTC
ACTACCCAGGAGAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAAACTTTTAAGAAGA
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

75)

ATGTCCAACGCCACCCTACTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCCCTCTTTGGAATCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTACCTCCACACCCCCATGTACTACTTCCTCA
CCAACTGTCTTCAATTGACATGTGGTTCTCCACTGTCACGGTGCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGACTATCTCTCCACAGCTGCGTGGCTCAGCTCTATTTTT
TCCACTTCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCCTATGATCGCTACCT
GGCCATCAGTTACCCGCTCAGGTACCAACATGATGACTGGGCGCTCGTGTGCCCTCCTG
GCCACGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTCC
ATTTGCCCTACTGTGGACCCAACCATCCAGCACTACTTCTGTGACGCACCGCCCATCT
GAAACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGAATATTGGGCTA
GTGGCCTCGGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCT
GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCATTACCTGAGGCCAGGCTCCAGGGACGC
CTTGCATGGGGTTGTGGCCGTTTTCTACACCACGCTGACTCCTCTTTCAACCCTGTTGTGT
ACACCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCAATAT
TTGCTCAGGGTGAATAG

(SEQ ID NO: 76)

(SEQ ID NO: 77)

ATGAACCTGAAACTGGACTCAGGTAACAAGCTTTGTCCTTCTGGGTTTCCCCAGTAGCC
ACCTCATACAGTTCCTGGTGTTCCTGGGGTTAATGGTGACCTACATTGTAACAGCCACAGG
CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCTGCACATACAGATGTACTTC

TTCCTGCGGAATTTCTCCTTCCTGGAGCTGTTGCTGGTAACTGTTGTGGTTCCCAAGATGCT
 TGTCGTCATCCTCACGGGGGATCACACCATCTCATTTGTGAGCTGCATCATCCAGTCCTACC
 TCTACTTCTTTCTAGGCACCACTGACTTCTTCTCTTGGCCGTCATGTCTCTGGATCGTTAC
 CTGGCAATCTGCCGACCACTCCGCTATGAGACCTGATGAATGGCCATGTCTGTTCCCAAC
 5 TAGTGCTGGCCTCCTGGCTAGCTGGATTCTCTGGGTCCTTTGCCCCACTGTCCTCATGGCC
 AGCCTGCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCTGTGACAGTTGGCCCTTGCT
 CAGGCTTTCTGTGGGGACACCCACCTGCTGAAACTGGTGGCTTTTATGCTCTCTACGTTG
 GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCTATGCCTGCATTCTTGCCACTGTTCT
 CAGGGCCCCCTACAGCTGCTGAGCGAAGGAAAGCGTTTCCACTTGCGCCTCGCATCTTACA
 10 GTGGTGGTCATCATCTATGGCAGTTCATCTTTCTCTACATTGCTATGTCAGAGGCTCAGTC
 CAAACTGCTCAACAAAGGTGCCTCCGTCCTGAGCTGCATCATCACACCCCTCTTGAACCCA
 TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTTGGGGTGGC
 CCAGGCTCACTGCTGTGATGAAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO:
 78)

15

AOLFR42 sequences:

MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSAVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL
 GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFHFIGGIKIFLLTMAYDRYIAISQPL
 HYTLIMNQTVCALLMAASWVGFIHSIVQIALTIQLPFCGPKLDNFYCDVPQLIKLACTDTFV
 20 LELLMVSNNGLVTLMCFLVLLGSYALLVMLRSHSREGRSKALSTCASHIAVVTILFVPCIYVY
 TRPFRTPMDKA VSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGLEHRPLH
 (SEQ ID NO: 79)

ATGAATCCAGCAAATCATTCCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT
 25 GGGAGCTTCGGTTTGTCTTCTTCTACTGTTTCTCTGCTGTGTATTTTATGACTGTAGTGGGA
 AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTTCT
 CTTGGGCAATCTTTCTTCTGGAATTTTGTACTCTTCCATCACAGCACCTAGGATGCTGG
 TTGACTTGCTCTCAGGCAACCCTACCATTTCCTTTGGTGGATGCCTGACTCAACTCTTCTTC
 TTCCACTTCATTGGAGGCATCAAGATCTTCTGCTGACTGTCATGGCGTATGACCGCTACA
 30 TTGCCATTTCCCAGCCCTGCACTACACGCTCATTATGAATCAGACTGTCTGTGCACTCCTT
 ATGGCAGCCTCCTGGGTGGGGGGCTTCATCCACTCCATAGTACAGATTGCATTGACTATCC
 AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACCTTTTATTGTGATGTGCCTCAGCTGAT
 CAAATTGGCCTGCACAGATACCTTTGTCTTAGAGCTTTTAATGGTGTCTAACAATGGCCTG
 GTGACCTGATGTGTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCATGCTCC
 35 GAAGCCACTCACGGGAGGGCCGAGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT
 GGTGACCTTAATCTTTGTGCCTTGATCTACGTCTATACAAGGCCCTTTTCGGACATTCCCCA
 TGGACAAGGCCGTCTCTGTGCTATACACAATTGTACCCCCATGCTGAATCCTGCCATCTA
 TACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG
 ACCCTATTGGTCCCCTGGAGCACAGACCCTTACATTAG (SEQ ID NO: 80)

40

AOLFR43 sequences:

MQKPQLLVPIIATSNGNLVHAA YFLLVGIPGLGPTIHFWLAFPLCFMYALATLGNLTIVLIIRVE
 RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIQEIEFNICLAQMFLIHLSAVESAVLLA
 MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFPLPFILKWLSYQCQHTVTHSFCLHQ
 45 DIMKLSCTDTRVNVVYGLFIHLSVMGVDSLFIGFSYILILWAVLELSSRAALKAFNTCISHLCAV
 LVFYVPLIGLSVVHRLGGPTSLHVVMAANTYLLLPVNVNPLVYGAKTKEICSRVLCMFSSQGGK
 (SEQ ID NO: 81)

ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG
 50 CAGCATACTTCCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACACTTTTGGCTGGCT
 TTCCCACTGTGTTTTATGTATGCCTTGGCCACCCTGGGTAACCTGACCATTGTCCTCATCAT
 TCGTGTGGAGAGGCGACTGCATGAGCCCATGTACCTCTTCTGGCCATGCTTTCCACTATT
 GACCTAGTCCTCTCCTCTATCACCATGCCCAAGATGGCCAGTCTTTTCTGATGGGCATCCA
 GGAGATCGAGTTCAACATTTGCCTGGCCAGATGTTTCTTATCCATGCTCTGTGAGCCGTG
 55 GAGTCAGCTGTCTGCTGGCCATGGCTTTTGACCGCTTTGTGGCCATTTGCCACCCATTGC
 GCCATGCTTCTGTGCTGACAGGGTGTACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG

WO 01/98526

GGGGTTTGTATTCTTCTTCCCACTGCCCTTCATCCTCAAGTGGTTGCTCTACTGCCAAACAC
 ATACTGTCACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCTGTACTGACAC
 CAGGGTCAATGTGGTTTATGGACTCTTCATCCTCTCAGTCATGGGTGTGGACTCTCTCT
 TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTTGGAGCTGTCCTCTCGGAGGGCA
 5 GCACTCAAGGCTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC
 CCTATTGGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCCACCTCCCTCCATGTGGTT
 ATGGCTAATACCTACTTGGTGTACACCTGTAGTCAACCCCTGTCTATGGAGCCAAGA
 CCAAAGAGATCTGTTCAAGGGTCTCTGTATGTTCTACAAGGTGGCAAGTGA (SEQ ID
 NO: 82)

10

AOLFR44 sequences:

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVMFNGCIVVFIVRTERS LHAPMYLFLC
 MLAIDLALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHP
 RHA AVLNNVTVAQIGIVAVVRGSLFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYADTL
 15 NVVYGLTAILVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLA FYVPLIGLS
 VVHRFGNSLHPVIRVVMGDIYLLPPVINPIHYGAKTKQIRTRVLAMFKISCDKDLQAVGGK
 (SEQ ID NO: 83)

ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA
 20 AAGCCCATTTCTGGGTGGCTTCCCCCTCCTTTCCATGTATGTAGTGCAATGTTTGGAAAC
 TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTC
 TCTGCATGCTTGCAGCCATTGACCTGGCCTATCCACATCCACCATGCCTAAGATCCTTGCC
 CTTTTCTGGTTTGATTCCCGAGAGATTAGCTTTGAGGCCTGTCTTACCCAGATGTTCTTTAT
 TCATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTTGACCGTTATGTGG
 25 CCATCTGCCACCCACTGCGCCATGCTGCAGTGTCTCAACAATACAGTAACAGCCAGATTGG
 CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTTTTCCCACTGCCTCTGCTGATCAAGCGG
 TGGCCTTCTGCCACTCCAATGTCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAA
 GTTGGCCTATGCAGACACTTTGCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGT
 ATGGGCGTGGACGTAATGTTTCATCTCCTTGTCTATTTTCTGATAATACGAACGGTCTGC
 30 AACTGCCTTCCAAGTCAGAGCGGGCCAAAGCCTTTGGAACCTGTGTGTACACATTGGTGT
 GGTACTCGCCTTCTATGTGCCACTTATGGCCTCTCAGTGGTACACCGCTTTGGAAACAGC
 TTTCATCCCATTTGTGCGTGTGTGATGACATCTACCTGCTGCTGCCTCCTGTATCAAG
 TCCCATCATCTATGGTGCCAAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG
 ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

35

AOLFR45 sequences:

MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIHQADAALHEPMYLFLA
 MLATIDLVLSTTLPKMLAIFWFRDQENFFACLVMFFLHSFSIMESA VLLAMAFDRYVAICKP
 LHYYTVLTGSLITKIGMAAVARAVTLMTPLPFLRRFHYCRGPVIAHCYCEHMAVVRACGDT
 40 SFNNIYGIAVAMFSVLDLLFVLSYVFILQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVVIS
 SVMHRVARHAAPRVHILLAIFYLLFPPMVNPIHYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:
 85)

TGGAAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTTGAACTCTAATCATATATA
 45 CTGTAGAAGGTATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTCCTA
 GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTGTGGTAGGAAT
 TCCTGGTTTGGAAACACCTGCATGCCTGGATCTCCATCCCCCTTCTGCTTGTCTATACTCTGG
 CCCTGCTAGGCAACTGTACCTTCTCTTATTATCCAGGCTGATGCAGCCCTCCATGAACCC
 ATGTACCTCTTTCTGGCCATGTTGGCAACCATGACTTGGTCTTTCTTCTACAACGCTGCC
 50 CAAAATGCTTGCCATATTCTGGTTCAGGGATCAGGAGATCAACTCTTTGCTGTCTGGT
 CAGATGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGTGCTGGCCATGGCCT
 TGACCGCTATGTGGCCATCTGCAAGCCATTGCACTACACGACGGTCTGACTGGGTCCCTC
 ATCACCAGATTGGCATGGCTGCTGTGGCCGGGCTGTGACACTAATGACTCCACTCCCTC
 TCCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCCATGCTACTGTGAACA
 55 CATGGCTGTGGTAAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATTGCT
 GTGGCCATGTTTAGTGTGGTGTGGACCTGCTCTTGTATCCTGTCTTATGCTTCTATCCT

TCAGGCAGTTCTCCAGCTTGCCTCTCAGGAGGCCCGCTACAAAGCATTGTTGGGACATGTGTG
 TCTACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCACCG
 TGAGCCCGCCATGCTGCCCCCTCGTGTCCACATACTCCTTGCTATTTTCTATCTCCTTTTCC
 CACCCATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTCGTGAGTATGTGCT
 5 CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTTTATCCCACTTGCCA
 AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAATTGCAGAGT
 ATCTTTGACAATTCTCTAGTATGATAAGGAAAAATGAGGTTTCATTCTCAGATCTACGA
 GTCAGGTCAAACCAGGAGTGCACCTATAGTCTGGTCTGATAGTAGAGGTTTGACCTTCCCA
 TTGTCATAGACTCATCATATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG
 10 GGTGAAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID
 NO: 86)

AOLFR46 sequences:

MNIKHCGWHMIHTWLNIREDDSDFKNFIGQIQGLSGNPHSTTSRMYFLCFCTSLLGFKVHWV
 15 SRLIXKLYMASPNDSTAPVSEFLICFPNFQSWQHWLSLPLSLLFLLAMGANTLLITIQLEAS
 LHQPLYLLSLLSLLDIVLCLTVIPKVLAIWFDFLRISFPACFLQMFIMNSFLTMESCTFMVMA
 YDRYVAICHPLRYPSTIDQFVARAVFVIARNAFVSLPVPMLSARLRYCAGNIKNCICSNLSVS
 KLSCDDITFNQLYQFVAGWTLLGSDLILIVISYFILKVVLRIKAEGAVAKALSTCGSHFILILFFS
 TVLLVLVITNLARKRIPDPVILLNHLHIPPALNPVYGVRTKEIKQGIQNLLKRL (SEQ ID NO:
 20 87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT
 GATGACAGTGATTTTAAAACTTTATTGGACAGATACAGGGCCTCAGTGAAACCCACACT
 CTACTACGTCTAGAATGTACTTTTTATGTTTCTGTACTTCTCTACTAGGTTTTAAGGTACAC
 25 TGGGTCTCCAGATTGATCANGAACTTTACATGGCATCTCCCAACAATGACTCCACTGCCC
 CAGTCTCTGAATTCCTCCTCATCTGCTTCCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT
 CTGCCCCCAGCCTTCTCTTCTCCTGGCCATGGGAGCTAACACCACCCTCCTGATCACCAT
 CCAGCTGGAGGCCTCTCTGCACCAGCCCCGTGACTACCTGCTCAGCCTCCTCTCCCTGCTGG
 ACATCGTGCTCTGCCTCACCGTCATCCCCAAGGTCCTGGCCATCTTCTGGTTTGACCTCAGG
 30 TCGATCAGCTTCCCAGCCTGCTTCTCCAGATGTTTCATCATGAACAGTTTTTTGACCATGGA
 GTCCTGCACGTTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA
 TACCCGTCTATCATCACTGACCAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA
 ATGCCCTTGTCTCTTCTCCTGTTCCCATGCTTTCTGCCAGGCTCAGATACTGTGCAGGAAAC
 ATAATCAAGAACTGCATCTGCAGTAACCTGTCTGTGTCCAACTCTCTTGTGATGACATCA
 35 CTTTCAATCAGCTCTACCAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT
 ATTGTTATCTCCTATTCTTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGCTGT
 GGCCAAGGCCTTGAGCACGTGTGGTTCCCACTTCATCCTCATCCTCTTCTTTCAGCACAGTCC
 TGCTGGTTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCCTCCAGATGTCCCCATCCT
 40 GCTCAACATCCTGCACCACCTCATTCCCCCAGCTCTGAACCCCATGTTTATGGTGTGAGA
 ACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

AOLFR47 sequences:

MSASNITLTHPTAFLLVGIPGLEHLHIWISIPFCLAYTLALLGNCTLLLIQADAALHEPMYLFLA
 MLAAIDLVLSSALPKMLAIFWFRDREINFFACLAQMFFLHSFSIMESAVLLAMAFDRYVAICK
 45 PLHYTKVLTGSLITKIGMAAVARAVTLMTPLPFLLRFCFHYCRGPVIAHCYCEHMAVVRACGD
 TSFNNIYGIAMFIVVLDLLLVLSYIFILQAVLLLASQEARYKAFGTCVSHIGAILAFYTTVVIS
 SVMHRVARHAAPHVHILLANFYLLFPPMVNPIIYGVKTKQIRESILGVFPRKDM (SEQ ID NO:
 89)

50 ATGTCAGCCTCCAATATCACCTTAACACATCCAACTGCCTTCTTGTGGTGGGGATTCCAG
 GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG
 CTTGGAACTGCACTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT
 ACCTCTTTCTGGCCATGTTGGCAGCCATCGACCTGGTCTTTCTCCTCCTCAGCACTGCCAAA
 55 ATGCTTGCCATATTCTGGTTTCAGGGATCGGGAGATAAACTTCTTTGCTGTCTGGCCAGG
 TGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGTGCTGGCCATGGCCTTTGAC
 CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCTGACTGGGTCCCTCATCA

CCAAGATTGGCATGGCTGCTGTGGCCCCGGGCTGTGACACTAATGACTCCACTCCCCTTCCT
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG
CCATGTTTATTGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTTATTCTTCAG
5 GCAGTTCTACTGCTTGCCCTCAGGAGGCCCGCTACAAGGCATTTGGGACATGTGTCTCTC
ATATAGGTGCCATCTTAGCCTTCTACACAAGTGTGGTCACTCTTCAGTCATGCACCGTGTA
GCCCCCATGCTGCCCCCTCATGTCCACATCCTCCTTGCCAAATTTCTATCTGCTCTCCCACC
CATGGTCAATCCCATAATCTATGGTGTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGA
GTATCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

10

AOLFR48 sequences:

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYVTRTEHSLHEPMYIFL
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFHLSLGMESTVLLAMAFDRYVAICH
PLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHQDVMKLACDDI
15 RVNVVYGLVHSAIGLDSLLISFSYLLIKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFGLSM
VHRFSKRDSPLPVILANIYLLVPPVLNPVYGVKTKAIRQLRLRFHVATHASEP (SEQ ID NO:
91)

20 ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC
CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTTGTGCTCCCTCTACCTTATTGCT
GTGCTAGGTAACCTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA
TGTATATATTTCTTTCATGCTTTTCAAGCATTGACATCCTCATCTCCACCTCATCCATGCC
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGTACA
GATGTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTTTT
25 GACCGCTATGTGGCCATCTGTACCCACTGCGCCATGCCACAGTACTTACGTTGCCTCGTG
TCACCAAAATTGGTGTGGCTGCTGTGGTGCGGGGGGCTGCACTGATGGCACCCCTTCTGT
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCCTACACC
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCTGCTATGGCCTTATCGT
CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATTCTTA
30 AGACTGTGTTGGGCTTGACACGTGAAGCCAGGCCAAGGCATTGGCACTTGGCTCTCTCA
TGTGTGTGCTGTGTTTCAATTTCTATGTACCTTTTATTGGATTGTCCATGGTGCATCGCTTA
GCAAGCGGCGTGACTCTCCGCTGCCCCGTATCTTGCCAATATCTATCTGCTGTTCTCCTCT
GTGCTCAACCAATTGTCTATGGAGTGAAGACAAAGGAGATTCGACAGCGCATCCTTCGA
CTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

35

AOLFR49 sequences:

MLTFHNVCSVPSSFWLGTGIPGLES�HVWLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF
LCMLAAIDLVLSTSTIPKLLGIFWFGACDIGLDACLGQMFLLHCFATVESGIFLAMAFDRYVAIC
NPLRHSMVLTYTVVGRGLVSLLRGVLYIGPLPLMIRLRLPLYKTHVISHSYCEHMAVVALT
40 GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKTGTGASHLCAILIFYVP
IAVSSLIHRFGQCVPPPVTLLANFYLLIPPILNPVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID
NO: 93)

45 ATGCTCACTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG
GCTGGAGTCCCTACACGTCTGGCTCTCCATCCCCCTTGGCTCCATGTACCTGGTGGCTGTG
GTGGGGAATGTGACCATCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACAGCCCATG
TACTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA
ACTTCTGGGAATCTTCTGGTTCGGTGCTTGTGACATTGGCCTGGACGCTGCTTGGGCCAA
ATGTTCTTATCCACTGCTTGGCACTGTTGAGTCAGGCATCTTCTTGGCATGGCTTTTGA
50 TCGCTACGTGGCCATCTGCAACCCACTACGTATAGCATGGTGTCACTTATACAGTGGTG
GGTCTTTGGGGCTGTTTCTCTCCTCCGGGGTGTCTCTACATTGGACCTTGCCTCTGAT
GATCCGCTGCGGCTGCCCTTTATAAAACCATGTTATCTCCACTCCTACTGTGAGCAC
ATGGCTGTAGTTGCCTTGACATGTGGCGACAGCAGGGTCAATAATGTCTATGGGCTGAGC
ATCGGCTTCTGGTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT
55 CAGGGCCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCTGGGGACATGCGC
TTCTCACCTCTGTGCCATCCTGATCTTTTATGTTCCCATTGCTGTTTCTCCTGATTCACCG

ATTTGGTCAGTGTGTGCCTCCTCCAGTCCACACTCTGCTGGCCAACTTCTATCTCCTCATTC
CTCCAATCCTCAATCCCATTGTCTATGCTGTTTCGCACCAAGCAGATCCGAGAGAGCCTTCT
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

5 **AOLFR50 sequences:**

MNLDSSFFSFLKSLIMALSNSSWRLPQPSFVLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII
WMDPSLHQSMYFLSMLAAIDLVASSTAPKALAVLLVRAQEIGYTVCLIQMFTHAFSSMES
GVLVAMALDRYVAICHPHLLHSTILHPGVIGHIGMVVLVRGLLLIPFLILLRKLIFCQATIIGHAY
CEHMAVVKLACSETTVNRAYGLTVALLVVGDLVLAIGVSYAHILQAVLKVPGNEARLKAFST
10 CGSHVCVILVFYIPGMFSFLTHRFGHHVPHHVHVLAILYRLVPPALNPLVYRVKTQKIHQ
(SEQ ID NO: 95)

ATGAATTTGGATTCTTTTTTCTCTTTCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC
CAGCTGGAGGCTACCCAGCCTTCTTTTTTCTGGTAGGAATCCGGGTTTAGAGGAAAGC
15 CAGCACTGGATCGCACTGCCCCCTGGGCATCCTTTACCTCCTTGCTCTAGTGGGCAATGTTA
CCATTCTCTTCATCATCTGGATGGACCCATCCTTGACCAATCTATGTACCTCTTCTCTGTCC
ATGCTAGCTGCCATCGACCTGGTTGTGGCCTCCTCCACTGCACCCAAAGCCCTTGCAGTGC
TCCTGGTTCTGTGCCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTCACCCAT
GCATTCTCCTCCATGGAGTCAGGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA
20 TTTGTACCCCTTGCACCATTCACAATCCTGCATCCAGGGGTCATAGGGGCACATCGGAAT
GGTGGTGTCTGGTGCGGGGATTACTACTCCTCATCCCCTTCTCATTCTGTTGCGAAAACCTT
ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAAC
TTGCCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGTCTGTGGT
TGGGCTGGATGTCTGGCCATTGGTGTTCCTATGCCACATTCTCCAGGCAGTGTCTGAAG
25 GTACCAGGAAATGAGGCCCGACTTAAGGCCTTTAGCACATGTGGCTCTCATGTTTGTGTCA
TCCTGGTCTTCTATATCCCGGAATGTTCTCCTTCTCACTCACCGCTTGGTTCATCATGTA
CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTGCCACCTGCACTCAATCC
TCTTGTCTATAGGGTGAAGACCCAGAAGATCCACCAGTGA (SEQ ID NO: 96)

30 **AOLFR51 sequences:**

MCQQILRDCILLIHLHCINRKKVSLVMLGPAYNHTMETPASFLLVGIPGLQSSHLWLAIISLSAM
YIALLGNTHIVTAIWMDSTRHEPMYCFCLVLAADVIMASSVVPKMVSIFCSGDSSISFSACFTQ
MFFVHLATAVETGLLLTMAFDYVAICKPLHYKRILTPQVMLGMSMAITIRAIITPLSWMVS
HLPFCGSNVVHSYCEHIALARLACADVPSSLYSLIGSSLMVGSVDVAFIAASYILKAVFGLSS
35 KTAQLKALSTCGSHVGMALYLPGMASIYAAWLGQDVVPLHTQVLLADLYVIIPATLNPITY
GMRTKQLRERIWSYLMHVLFDHNSLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTGTGTGATTAAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
40 CTTCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTAGGAAACACCATCATCGTGAAGCAATCTGGATGGA
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
45 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
GCAGTCTCTACAGTCTGATTGGTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
50 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGGCCTTGACACCCCAAGTCCTGC
TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
CAAACAACCTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATCCAAC
55 CTGGGTTTCATGA (SEQ ID NO: 98)

AOLFR52 sequences:

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISSLAMYITALLGNTLIVTAIWMDSTRHEPMY
 CFLCVLAAVDIVMASSVVPKMVSIFCSGSSISFSACFTQMFFVHLATAVETGLLLTMAFDYRV
 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMMNHLPCGSNVVHSHYCKHIALAR
 5 LACADVPVSSLYSLIGSSLMVGSDFVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGVMAly
 YLPGMASIYAAWLQDIVPLHTQVLLADLYVIIPATLNPITYGMRTKQLLEGIWSYLMHFDFH
 SNLGS (SEQ ID NO: 99)

10 ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTTCCTCCTGTGGGTA
 TCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC
 AGCCCTGTTAGGAAACACCCTCATCGTGACTGCAATCTGGATGGATTCCACTCGGCATGAG
 CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCCGTGGT
 ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTC
 15 ACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATG
 CTTTGGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCAGCCTCA
 AGTGATGCTGGGAATGAGTATGGCCGTCAACATCAGAGCTGTCACATTGACTCCACTG
 AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCCTACTGTAA
 GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCGTGCCAGCAGTCTCTACAGTCTG
 ATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT
 20 TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAAGCACATGT
 GGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATGGCATCCATCTATGCGG
 CCTGGTTGGGGCAGGATATAGTGCCCTTGACACCCAAGTGCTGCTAGCTGACCTGTACGT
 GATCATCCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAACAATTGCTGGAG
 GGAATATGGAGTTATCTGATGCACTTCTCTTTGACCACTCCAACCTGGGTTTCATGA (SEQ
 25 ID NO: 100)

AOLFR54 sequences:

MSDSNLSDNHLPDFTFLTGIPGLEAAHFWIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY
 LFLCLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVA
 30 ICNPLRYTTILNHAVIGRIGFVGLFRSVAIVSPFILLRRLPYCGHRVMTHTYCEHMGARLACA
 NITVNIVYGLTVALLAMGLDSILIAISYGFIHAFVHLPSHDAQHKALSTCGSHIGILVFIYPAFF
 SFLTHRFHHEVPKHVHIFLANLYVLVPPVLNPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID
 NO: 101)

35 ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC
 CAGGGCTGGAGGCTGCCACTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTTGTAGC
 ACTGGTTGGAATGCTGCCCTCATCTGGTCATTGCCATGGACAATGCTCTTCATGCACCT
 ATGTACCTCTTCTCTGCTTCTCTCACTCACAGACCTGGCTCTCAGTTCTACCACTGTGCC
 CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCCTTTGGTGGATGCCTGGCC
 40 CAGATGTTTTGTGTCCATTCTATCTATGCTCTGGAGTCTCGATTCTACTTGCCATGGCCTT
 TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATAACAACATTCTCAACCATGCTGTC
 ATAGGCAGAATTGGCTTTGTTGGGCTATTCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT
 CTTGCTGAGGCGACTCCCCTACTGTGGTCACCGTGTGATGACACACATACTGTGAGCAT
 ATGGGCATCGCCCGACTGGCCTGTGCCAATCACTGTCAATATTGTCTATGGGCTAACTG
 45 TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTCTCTATGGCTTTATCCTC
 CATGCAGTCTTTCACCTTCCATCTCATGATGCCAGCACAAGCTCTGAGTACCTGTGGCT
 CCCACATTGGCATCATCCTGGTTTTCTACATCCCTGCCTTCTTCTCCTTCTCACCACCGC
 TTTGGTCACCACGAAGTCCCCAAGCATGTGCACATCTTCTGGCTAATCTCTATGTGCTGG
 TGCTCCTGTACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTGCGAGTCGACT
 50 TCTAAAACCTGCTTCACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

AOLFR57 sequences:

MSFQVVTYMFYLHWTMEKSNNSTLFILLGFSQNKNEI VLCFVLFYIAIWMGNLLIMISITCTQ
 LIHQPMYFFLNYLSLSDLCYTSTVTPKLMVDLLAERKTISYNNCMIQLFTTHFFGGIEIFLTGM
 55 AYDRYVAICKPLHYTIIMSQRKCNTHVCCCTGGFIHSASQFLLTIFVPCGPNEDHYFCDVYPLL
 KLACSNHIMIGLLVIANSGLIALVTFVLLSYVFILYTIIRAYSAERRSKALATCSSHVIVVLF

APALFIYIRPVTTFSEDKVFALFYTHIAPMFNPLIYTLRNTEMKNAMRKVWCCQILLKRNQLF
(SEQ ID NO: 103)

5 ATGTCATTTTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAGCAATAATA
GCACTTTGTTTATTCTCTTGGGGTTTTCCCAAATAAGAACATTGAAGTCCTCTGCTTTGTA
TTATTTTTGTTTTGCTACATTGCTATTTGGATGGGAACTTACTCATAATGATTTCTATCAC
GTGCACCCAGCTCATTACCAACCCATGTATTTCTTCCTCAATTACCTCTCACTCTCCGACC
TTTGCTACACATCCACAGTGACCCCCAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC
10 CATTTCTATAATAACTGTATGATACAACTCTTTACCACCCATTTTTTTGGAGGCATAGAGA
TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTGCAAGCCCCTGCACTA
CACCATTATTATGAGCAGGCAAAAGTGTAACACAATCATCATAGTTTGTGTACTGGGGGA
TTTATACATTCTGCCAGTCAGTTTCTTCTCACCATCTTTGTACCATTTTTGTGGCCCAAATGA
GATAGATCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA
TGATAGGTCTCTTAGTCATTGCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTTGTCTTG
15 TTGTTGTCTTATGTTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA
AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCCTGTTTTTGTCTCTGCATTG
TTCATTTACATTAGACCGGTCACAACATTCTCAGAAGATAAAGTGTTTGCCTTTTTTATAC
CATCATTGCTCCCATGTTCAACCCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC
GCCATGAGGAAAGTGTGGTGTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA (SEQ
20 ID NO: 104)

AOLFR58 sequences:

MFSTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQNPVQEIFVVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
25 TPKMIVDSLVTYTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINS
FICIINFSLLLVSAYAVILLSLRTHSSEGRWKALSTCGSHLAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLNPLIYTFRNKEVKQAMRRIWNRLMVVSEKENIKL (SEQ ID NO: 105)

30 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTTGCACTTGGATGTACCAACTTGTTAA
TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCCTTTGTCCTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTTCATCTTTTCCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCCTGCGGACTTTACAGAAATCCAAATGTTCAAGAAATAGTATTTGTTG
TATTTTTGTTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCAATTCTC
35 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCTTCTGGA
TGCCTGCTTCTCATCTGTATCACCACAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
40 GGCTCTTGCATTCCATGATACAAATCTTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTATCTTGTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
45 TATTTGTATATACACGACCTCCATCTGCTTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTACACTTTCAGGAATAAGGAAGTAAAC
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 106)

AOLFR59 sequences:

MGDWNNSDAVEPIFILRGFPGLLEYVHWSLSILFCLAYLVAFMGNVTILSVIWISSLHQPYYFI
SILAVNDLGMSTLPTMLAVLWDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH
PLHYPTILTNSVIGKIGLACLLRSLGVVLPPLLLRHYHYCHGNALSHAFCLHQDVLRSLCTDA
RTNSIYGLCVVIATLGVDISIFILLSYVLIILNTVLDIASREEQLKALNTCVSHICVVLFFVPVIGVS
55 MVHFRFGKHLSPIVHILMADIYLLPVLNPIVYSVRTKQIRLGILHKFVLRRLF (SEQ ID NO:
107)

ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTCTCTG
GACTGGAGTATGTTCACTTCTGGCTCTCCATCCTCTTCTGTCTGCATATTTGGTAGCATT
ATGGGTAATGTTACCATCCTGTCTGTCAATTTGGATAGAATCCTCTCTCCATCAGCCCATGTA
5 TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCCACCA
TGCTTGCTGTGTTATGGTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGCTATGCTCAGCT
GTTCTTCATCCACACATTCACATTCCTGGAGTCCCTCAGTGTTGCTGGCCATGGCCTTTGACC
GTTTTGTTGCTATCTGCCATCCACTGCACTACCCACCATCCTACCAACAGTGTAATTGGC
10 AAAATTGGTTTGGCCTGTTTGTACGAAGCTTGGGAGTTGTACTTCCCACACCTTTGCTACT
GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCACGCCTTCTGTTTGCACCAAGGAT
GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA
TTGCCACACTAGGTGTGGATTCAATCTTCATACTTCTTTCTTATGTTCTGATTCTTAATACT
GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCACTCAACACATGTGTATCCCAT
TCTGTGTGGTGCTTATCTTCTTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG
15 AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTCCCCCAGT
CCTTAACCCTATTGTCTATAGTGTGAGAACAAGCAGATTCTGCTAGGAATTCTCCACAAG
TTTGTCTAAGGAGGAGGTTTTAA (SEQ ID NO: 108)

AOLFR60 sequences:

20 MFPLNDTQFHPSSFLLLGIPGLETLHIWIGFPFCVYMIALIGNFTILLVIKTDSSLHQPMFYFLA
MLATTDVGLSTATIPKMLGIFWINLRGIIEAQLTQMFFIHNFTLMESAVLVAMAYDSYVAICN
PLQYSAILTNKVVSIGLVFVRALIFVIPSILLILRLPFCGNHVIPHTYCEHMGHLASCAIKINI
IYGLCAICNLVFDITVIALSYVHILCAVFRLPHEPRLKSLSTCGSHVCVILAFYTPALFSFMTHC
FGRNVPRYIHILLANLYVVVPPMLNPVIYGVRTKQIYKCVKKILLQEQGMEKEEYLIHTRF
25 (SEQ ID NO: 109)

ATGTTCTTCCCAATGACACCCAGTTTCACCCCTCCTCCTTCTGTTGCTGGGGATCCCAGG
ACTAGAAACACTTCACATCTGGATCGGCTTTCCTTCTGTGTACATGATCGCACTC
ATAGGGAACTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCTACACCAGCCCATGT
30 TCTACTTCTGGCCATGTTGGCCACCACTGATGTGGGTCTCTCAACAGCTACCATCCCTAA
GATGCTTGGAACTTCTTGGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCACCCAG
ATGTTTTTTATCCACAACCTCACACTTATGGAGTCAGCAGTCCTTGTGGCAATGGCTTATG
ACAGCTATGTGGCCATCTGCAATCCAATATAAGCCATCCTACCAACAAGGTTGT
TTCTGTGATTGGTCTTGGTGTGTTTGTGAGGGCTTTAATTTTCGTCATTCCCTCTATACTC
35 TTATATTGCGGTGCCCTTCTGTGGGAATCATGTAATCCCCACACCTACTGTGAGCACAT
GGGTCTTGCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTTATGTTTATGTGCCA
TTTGTAATCTGGTGTGTTGACATCACAGTCATTGCCCTCTCTTATGTGCATATTCTTTGTGCT
GTTTTCCGCTTCTACTCATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTTCACATGT
GTGTGTAATCCTTGCTTCTATACACCAGCCCTCTTTCTTTATGACTCATTGCTTTGGCC
40 GAAATGTGCCCCGCTATATCCATATACTCCTAGCCAATCTCTATGTTGTGGTGCCACCAAT
GCTCAATCCTGTCATATATGGAGTCAGAACAAGCAGATCTATAAATGTGTAAAGAAAAT
ATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA
(SEQ ID NO: 110)

AOLFR61 sequences:

45 MSIINTSYVEITTFVLVGMPPLEYAHIWISIPICSMYLIAILNGNTILFIKTEPSLHGPMYYFLSML
AMSDLGLSLSSLPTVLSIFLNAPETSSSACFAQEFFIHGFSVLESSVLLMSFDRFLAIHNPLRYT
SILTTVRVAQIGIVFSFKSMMLVLPFPFTLRSLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
GFFGALCLMVDFILIAVSYTLILKTVPGIASKKEELKALNTCVSHICAVIIFYLPINLAVVHRFAG
50 HVSPLINVLMANVLLLVPPLMKPIVYCVKTKQIRVRVVAKLQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTGTTGGGATGCCAG
GGCTAGAAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCCATGT
55 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCCACT
GTGTTAAGCATCTTCTGTTCAATGCCCTGAACTTCTTCTAGTGCCTGCTTTGCCAGGA

ATTCTTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA
 GATTCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
 TAAGAAAGCTTGAGATATTGCAAGAAAAACCAATTATCCCATTCTACTGTCTCCACCAGGA
 5 TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
 ACCGGGAATTGCATCCAAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTACACATC
 TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCGG
 GCATGTCTCTCCCCTCATTAAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCGCTGA
 10 TGAAACCAATTGTTTATTGTGTAATAAATAACAGATTAGAGTGAGAGTTGTAGCAAAATT
 GTGTCAATGGAAGATTTAA (SEQ ID NO: 112)

AOLFR62 sequences:

MFYHNKSIFHPVTFFLIGIPGLEDFHFWISGPFCSVYLVALLGNAITILLVIKVEQTLREPMFYFL
 15 AILSTIDLALSATSVPRMLGIFWFDHEINYGACVAQMFLIHAFTGMEAEVLLAMAFDRYVAIC
 APLHYATILTSVLVGISMCIIVRPVLLTLPVYLIYRLPFCQAHIIAHSYCEHMGIAKLSCGNIRI
 NGIYGLFVVSFFVLNLVLIGISYVYILRAVFRLPASHDAQLKALSTCGAHVGVICVFYIPSVFSFLT
 HRFQHQIPGYIHILVANLYLIIPPSLNPIHYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

20 ATGTTTTATCACAACAAGAGCATATTTACCCAGTCACATTTTCTCCTCATTGGAATCCCAGG
 TCTGGAAGACTTCCACATGTGGATCTCCGGGCCCTTCTGCTCTGTTTACCTTGTGGCTTTGC
 TGGGCAATGCCACCATCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGCCCATGTT
 CTACTTCTGGCCATTCTTTCCACTATTGATTTGGCCCTTCTGCAACCTCTGTGCCTCGCA
 TGCTGGGTATCTTCTGGTTGATGCTCAGGAGATTAAGTATGGAGCTTGTGTGGCCAGAT
 25 GTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC
 CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTTGGT
 GGGCATTAGCATGTGCATTGTAATTCGTCCCGTTTTACTTACACTTCCCATGGTCTATCTTA
 TCTACCGCTACCCTTTTGTGAGGCTCACATAATAGCCCATTCCTACTGTGAGCACATGGG
 CATTGCAAAATTGTCTGTGGAAACATTCGTATCAATGGTATCTATGGGCTTTTTGTAGTTT
 30 CTTCTTTGTTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC
 TTCCGCCTCCCATCACATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTG
 GAGTCATCTGTGTTTTCTATATCCCTTCACTCTTCTCTTTCTTACTCATCGATTGAGACAC
 CAAATACCAGGTTACATTCACATTCTTGTGCAATCTCTATTTGATTATCCCACCTCTCT
 CAACCCCATCATTTATGGGGTGAGGACCAACAGATTTCGAGAGCGAGTGCTCTATGTTTTT
 35 ACTAAAAATAA (SEQ ID NO: 114)

AOLFR63 sequences:

MSIINTSYVEITTFVLVGMPLGEYAHIWISIPICSMYLIAILGNGTILFIKTEPSLHEPMYYFLSML
 AMSDLGLSLSSLPTVLSIFLNAPEISSNACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYTS
 40 ILTTVRVAQIGIVFSFKSMMLVLPFPFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
 GFFGALCLMVDFILIAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYLPINLAVVHRFAR
 HVSPLINVLMANVLLLVPPLTNPIVYCVKTKQIRVRVVAKLCQRKI (SEQ ID NO: 115)

45 ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
 CTAGGAAATGGCACCATTTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCATGT
 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT
 GTGTTAAGCATCTTCTGTTCAATGCTCCTGAAATTCATCCAATGCCTGCTTTGCCAGGA
 50 ATTCTTCATTATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA
 GATTCTAGCCATCCACAACCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
 TAAGAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCTACTGTCTCCACCAGGA
 TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
 55 ACTGGGAATTGCATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTGTTTACACATC
 TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG

GCATGTCTCTCCCCTCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA
CGAACCCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAAT
GTGTCAACGGAAGATTAA (SEQ ID NO: 116)

5 AOLFR64 sequences:

MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLTVILGNLTILHVICTDATLHGPMYYFLG
MLAVTDLGLCLSTLPTVLGFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL
HDSTVLTACIVKMGSSVLRALLPLPFLKRFQYCHSHVLAHAYCLHLEIMKLACSSIIVN
HIYGLFVVACTVGVDSLIFLSYALILRTVLSIASHQERLRALNTCVSHICAVLLFYIPMIGLSLV
10 HRFGEHLPRVHFLFMSYVYLLVPPLMNPPIYSIKTKQIRQRIKKFQFIKSLRCFWKD (SEQ ID
NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTTCTGACGGGCTTCCAAG
GTCTAGAAGGTCTCCATGGCTGGATCTCTATTCCCTTCTGCTTCATCTACCTGACAGTTATC
15 TTGGGGAACCTCACCATTCTCCACGTCATTTGTACTGATGCCACTCTCCATGGACCCATGT
ACTATTTCTTGGGCATGCTAGCTGTACAGACTTAGGCCTTTGCCTTTCCACACTGCCCCT
GTGCTGGGCATTTTCTGGTTTGATACAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC
TCTTCTTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC
CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCTGACACCTGCATGTATTG
20 TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCTTGCCTTCCCT
CTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATTGTCTTCACTGGA
GATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTTGTGTG
GCCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTTCTCTACAGCCCTCATCCTTCGCAC
CGTGCTCAGCATTGCCTCCCACAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT
25 ATCTGTGCTGACTGCTCTTCTACATCCCCATGATTGGCTGTCTTGTGCATCGCTTTGG
TGAACATCTGCCCCGCTGTACACCTCTCATGTCCTATGTGTATCTGCTGGTACCACCCC
TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCGCCAGCGCATCATTAAGAA
GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

30 AOLFR65 sequences:

MAGRMSTSNHTQFHPSSFLLLIGIPGLEDVHIWIGVPFFVYLVALLGNTALLFVIQTEQSLHEPM
YYFLAMLDSIDLGLSTATIPKMLGIFWFNTKEISFGGCLSHMFFIHFFTAMESIVLVAMAFDRYI
AICKPLRYTMILTSKISLAGIAVLRSLYMVVPLVFLLLRPLFCGHRIIPHTYCEHMGARLACAS
IKVNIRFGLGNISLLLDVILILSYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL
35 THREGHNIPQYIHILANLYVVVPPALNPVIYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCCATCCTTCTTCATTCTACTGCT
GGGTATCCCAGGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTCTTTGTGTAT
CTTGTTGCACTCCTGGGAAACACTGCTCTCTGTTTGTGATCCAGACTGAGCAGAGTCTCC
40 ATGAGCCTATGTACTACTTCTGGCCATGTTGGATTCCATTGACCTGGGCTGTCTACAGC
CACCATCCCCAAAATGTTGGGCATCTTCTGTTCAATACCAAAGAAATATCTTTTGGAGGC
TGCCCTTCTCACATGTTCTTCAATCTTCACTGCTATGGAGAGCATTGTGTTGGTGGC
CATGGCCTTTGACCGCTACATTGCCATTGCAAACCTCTTCGGTACACCATGATCCTCACCA
GCAAAATCATCAGCCTCATTGCAGGCATTGCTGTCTGAGGAGCCTGTACATGGTTGTTC
45 ACTGGTGTCTCTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTATT
GTGAGCATGGGCATTGCCCCTGTGGCAGCATCAAAGTCAACATTAGGTTTGG
CCTTGGCAACATATCTCTTGTACTGGATGTTATCCTTATTCTCTCTATGTGAGGA
TCCTGTATGCTGTCTTCTGCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGT
GGTCTCATATTGGTGTATCTTAGCCTTTTTACACCAGCATTTTTCTTCTGACACA
50 TCGTTTTGGCCATAATATCCACAGTATATACATATTATAGCCAACCTGTATGTGGTTG
TCCACAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTTCGAGAGAGAG
TGCTGAGGATTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

AOLFR66 sequences:

55 MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFL
ALLSFTDVLMCTSTLPNTLFILWFNLKEIDFKACLAQMFFVHTFTGMESGVLMMLMALDHCVAI

CFPLRYATILTNSVIAKAGFLTFLRGVMLVIPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN
VRVNAIYGLIVALLIGGFILCITISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF
TFFTHHFGGHTIPLHIHIMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGDNSHNF (SEQ
ID NO: 121)

5

ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTCATCCTAAATGGCATCCCTG
GTTTGGAAGATGTGCATTTGTGGATCTCCTTCCCACTGTGTACCATGTACAGCATTGCTATT
ACAGGGAACTTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT
ATGTCCTTCCCTGCCCTTCTTCCCTCACAGATGTGCTCATGTGCACCAGCACCTTCCCAAC
10 ACTCTCTTCATATTGTGGTTAATCTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCCAGAT
GTTCTTTGTGCACACCTTCACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGAC
CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAGTCATTGC
TAAAGCTGGGTTCCCTCACTTTTCTTAGGGGTGTGATGCTTGTTATCCCTTCCACTTTCCTCA
CCAAGCGCCTTCCATACTGCAAGGGCAACGTCATACCCACACCTACTGTGACCACATGTC
15 TGTGGCCAAGATATCTTGTGGTAATGTGAGGGTTAACGCCATCTATGGTTTGATAGTTGCC
CTGCTGATTGGGGGCTTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC
AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCAGCACCTGCACTGCCCAC
TTCTGTGCCATAGTCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCATTTTGG
GGGACACACCATTCCTCTACACATACATATTATTATGGCTAATCTCTACCTACTAATGCCTC
20 CCACAATGAACCCTATTGTGTATGGGGTGAACCAGGCAGGTACGAGAAAGTGTCTATTA
GGTTCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

AOLFR67 sequences:

MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYIIA VVGNCGLICLISHEEALHRPMYYFLA
25 LLSFTDVTLCCTMVNMLCIFWFNLKEIDFNACLAQMFFVHMLTGMESGVMLMALDRYVAI
CYPLRYATILTNPVIAKAGLATFLRNVMLIIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN
FKVNAIYGLMVALLIGVFDICISVSYTMILQAVMSLSSADARHKAFSTCTSHMCSIVITYVAAF
FTFFTHRFVGHNPNIHIIIVANLYLLLPPTMNPVYGVKTKQIQEGVIKFLGDKVVSFTYDK
(SEQ ID NO: 123)

30

ATGTCTGGGGACAACAGCTCCAGCCTGACCCAGGATTCTTTATCTTGAATGGCGTTCCTG
GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGCTGTC
GTGGGGAAGTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACCGGCCCATGT
ACTACTTCCCTGGCCCTGCTCTCCTTCACTGATGTACCTTGTGCACCACCATGGTACCTAAT
35 ATGCTGTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCCAGA
TGTTTTTTGTCCATATGCTGACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGA
CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG
CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCCATTCCTCTCCTC
ACCAAGCGCCTGCCCTATTGCCGGGGGAACCTTCATCCCCACACCTACTGTGACCATATGT
40 CTGTGGCCAAGGTATCCTGTGGCAATTTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC
TCTCCTGATTGGTGTGTTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGCAGG
CTGTTATGAGCCTGTCATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA
CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTTCACTTTTTTCACTCATCGTTTTGT
AGGACACAATATCCCAAACCATACACATCATCGTGGCCAACCTTTATCTGCTACTGCCT
45 CCTACCATGAACCCAATTGTTTATGGAGTCAAGACCAAGCAGATTACAGGAAGGTGTAATTA
AATTTTACTTGGAGACAAGGTTAGTTTACCTATGACAAATGA (SEQ ID NO: 124)

AOLFR68 sequences:

MTTHRNDTLSTEASDFLLNCFVRSPSWQHWLSLPLSLFLAVGANTLLMTTWLEASLHQPL
50 YYLLSLLSLDIVLCLTVIPKVLTFWFDLRPISFPACFLQMYIMNCFLAMESCTFMVMA YDRY
VAICHPLRYPSIITDHFVVKAAMFILTRNVLMTLPIPLSAQLRYCGRNVIENCICANMSVRLSC
DDVTINHL YQFAGGWTLGSDLILFLSYFILRAVRLKAEGAVAKALSTCGSHFMLILFFSTIL
LVFVLTHVAKKVS PDVPVLLNVLHHVIPAALNPIHYGVRTQEIKQGMQRLLKKGK (SEQ ID
NO: 125)

55

WO 01/98526

ATGACAACACACCGAAATGACACCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT
 TTGTCAGATCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCCCAGCCTCCTTTCTCTTG
 GCCGTAGGGGCCAACACCACTCTGATGACCATCTGGCTGGAGGCCTCTCTGCACCAGC
 CCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGACATCGTGCTCTGCCTCACTGTCATC
 5 CCCAAGGTCCTGACCATCTTCTGGTTTGACCTCAGGCCCATCAGCTTCCCTGCCTGCTTCT
 CCAGATGTACATCATGAATTGTTCTAGCCATGGAGTCTTGCACATTCATGGTCATGGCC
 TATGATCGTTATGTAGCCATCTGCCACCACTGAGATATCCATCAATCACTGATCACTT
 TGATGCAAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCCATCCCC
 ATCCTTTCAGCACAACTCCGTTATTGTGGAAGAAATGTCATTGAGAACTGCATCTGTGCCA
 10 ATATGTCTGTTTCCAGACTCTCCTGCGATGATGTCACCATCAATCACCTTACCAATTTGCT
 GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCTCCTACACCTTCATTCT
 GCGAGCTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAAGCACATGTGG
 CTCCCACTTCATGCTCATCCTCTTCTCAGCACCATCCTTCTGGTTTTTGTCTCACACATGT
 GGCTAAGAAGAAAGTCTCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCATT
 15 CCTGCAGCCCTTAACCCCATCATTTACGGGTGAGAACCAAGAAATTAAGCAGGGAATG
 CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

AOLFR69 sequences:

MSYSIYKSTVNIPLSHGTVHSFCHNMNCNFMHIFKVLDFNMKNVTEVTLFVLKGFTDNLELQ
 20 TIFFFLFLAIYLFITLMGNLGLILVVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN
 KVISFLGCV AQVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVMSPRVYVPLINASYVAGI
 LHATHTVATFSLFCGANEIRRVFCPIPLLAISYSDHTNQLLLFYFVGSIELVTILVLISYGLIL
 LAILKMYSAEGRRKVFSTCGAHLTGVSIIYGTILFMYVRPSSSYASDHDIMVSIFYTIVIPLLNPV
 IYSLRNKDVKDSMKMFGKNQVINKVYFHTTK (SEQ ID NO: 127)

25 ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCTTGAGTCATGGTGTGTTTCATT
 CTTTTGTGCATAATATGAAGTGAACCTTATGCATATCTTCAAGTTTGTCTAGATTTCAAC
 ATGAAGAATGTCAGTGAAGTTACCTTATTTGTACTGAAGGGCTTCACAGACAATCTTGAAC
 30 TGCAGACTATCTTCTTCTCCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTA
 GGACTGATTTTAGTGGTCAATTAGGGATTCCCAGCTCCACAAACCCATGTAATTTTCTGA
 GTATGTTGTCTTCTGTGGATGCCTGCTATTCTCAGTATTACCCCAAATATGTTAGTAGAT
 TTTACGACAAAGAATAAAGTCATTTCACTTCTGATGTGTAGCACAGGTGTTTCTTGCTT
 GTAGTTTTGGAACACAGAATGCTTCTTCTGGCTGCAATGGCTTATGATCGCTATGTAGC
 CATCTACAACCTCTCCTGTATTCACTGAGCATGTCACCCAGAGTCTACATGCCACTCATC
 35 AATGCTTCTATGTTGCTGGCATTTCATGCTACTATACATACAGTGGCTACATTTAGCCT
 ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTGTGATATCCCTCCTCTCCTTGCTA
 TTTCTTATTCTGACACTCACACAAACAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG
 CTGGTCACTATCCTGATTGTTCTGATCTCCTATGGTTTGATTCTGTTGGCCATTCTGAAGAT
 GTATTCTGCTGAAGGGAGGAGAAAGTCTTCTCCACATGTGGAGCTCACCTAAGTGGAGT
 40 GTCAATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTTCAGCTATGCTTCG
 GACCATGACATGATAGTGTCAATATTTACACCATTGTGATTCCCTTGCTGAATCCCGTCAT
 CTACAGTTTGAGGAACAAAGATGTAAAGACTCAATGAAAAAATGTTTGGGAAAAATCA
 GGTATCAATAAAGTATATTTTCATACTAAAAAATAA (SEQ ID NO: 128)

AOLFR70 sequences:

45 MDSTFTGYNLNLQVKTEMDKLSSGLDIYRNPLKNKTEVTMFILTGFTDDFELQVFLFLFFAI
 YLFTLIGNLGLVVLVIEDSWLHNPMMYYFLSVLSFLDACYSTVTPKMLVNFLAKNKSISFIGCA
 TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVMSPRVYVPLITASVYAGILHATHIVA
 TFLSFCGSNEIRHVFCMPPLAISCSHTHTNQLLLFYFVGSIEIVTILVLISCDIFILLSILKMHS
 50 KGRQKAFSTCGSHLTGVTHGTLVSYMRPSSSYASDHDIIVSIFYTIVIPKLNPIIYSLRNKEVK
 KAVKKMLKLVYK (SEQ ID NO: 129)

55 ATGGACTCCACTTTCACAGGCTATAACCTTTATAACCTGCAAGTAAAACTGAAATGGACA
 AGTTGTGTCAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCACCA
 TGTATATATTGACAGGCTTCACAGATGATTTTGTAGCTGCAAGTCTTCTATTTTACTATTT
 TTTGCAATCTATCTTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG

ATTCCTGGCTCCACAACCCCATGTATTATTTTCTTAGTGTTTTATCATTCTTGGATGCTTGC
 TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTTGGCAAAAAATAAATCCATTT
 CATTTATCGGATGTGCAACACAGATGCTTCTTTTTGTTACTTTTGGAACTACAGAATGTTTT
 CTCTTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCTCTCCTGTATTCACT
 5 GAGCATGTCAACCCAGAGTCTATGTGCCACTCATCACTGCTTCCTACGTTGCTGGCATTTTAC
 ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCTTCTGTGGATCCAATGAAATTAG
 GCATGCTTTTTGTGATATGCCTCCTCTCCTTGCTATTTCTTGTCTGACACTCACACAAACC
 AGCTTCTACTCTTCTACTTTGTGGGTCTATTGAGATAGTCACTATCCTGATTGTCCTCATT
 TCCTGTGATTTTCACTTCTGTTGTCCATTCTGAAGATGCATTCTGCTAAGGGAAGGCAAAAGG
 10 CCTTCTCTACATGTGGCTCTCACCTAAGTGGAGTGACAATTTATCATGGAACAATTCTCGTC
 AGTTATATGAGACCAAGTTCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATTTT
 ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAA
 AAAGGCAGTGAAGAAAATGTTGAAATTGGTTTACAAATGA (SEQ ID NO: 130)

15 **AOLFR71 sequences:**

MGRNNTNVPDFILTGLSDSEEVQMALFILLLIYLITMLGNVGMILIRLDLQLHTPMYFFLTH
 LSFIDLSYSTVITPKTLANLLTSNYISFMGCFQMFVFLGAAECFLSSMAYDRYVAICSPRLY
 PVIMSKRLCCALVTGPYVISFINSFVNVMWSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEI
 MIHILAGSTLMVSLITISASYVSILSTILKINSTSGKQKALSTCASHLLGVTFYGTMIFTYLPKPRK
 20 SYSLGRDQVASVFYTIVIPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

ATGGGTAGAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG
 AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGC
 AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATTTT
 25 TCCTTACTCACTTGTCACTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAAACCTTA
 GCGAAGTACTGACTTCCAATATATTTCTTCTGCTGGGCTGCTTTGCCAGATGTTCTTTTT
 TGTCTTCTTGGGAGCTGCTGAATGTTTTCTTCTCTCATCAATGGCCTATGATCGTCTACGTAG
 CTATCTGCAGTCTCTACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTC
 ACTGGGCCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC
 30 TGCATTTCTGCGACTCAAATGTAGTTCGTCATTTTCTGCGACACGTCTCCAATTTTAGCT
 CTGTCTGTCATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCCACCC
 TGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTTACCATCTGAAA
 ATTAATTCCTTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCCTCTCATCTCTTGGGAG
 TCACCATCTTTTATGGAAGTATGATTTTACTTATTTAAAACCAAGAAAGTCTTATTCTTTG
 35 GGAAGGGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT
 TTATAGTCTTAGAAACAAAGAAGTTAAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA
 GGACTCCAGGTAA (SEQ ID NO: 132)

AOLFR72 sequences:

40 MAPENFTRVTEFILTVSSCPQLIPLFLVFLVLYGLTMAGNLGIITLTSVDSRLQTPMYFFLQHL
 ALINLGNSTVIAPKMLINFLVKKKTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL
 YMVVSRRLCLLLVSLTYLYGFSTAIVVSSYVFSVSYCSSNIINHFCNDVPLLALSCSDTYLPE
 TVVFISAATNVVGSLLIIVLSYFNIVLSILKICSSEGRKKAFTSCASHMMAVTIFYGTLLFMYVQP
 RSNHSLDTDDKMASVFYTLVIPMLNPLIYSLRNKDVKTALQRFMTNLCYSFKTM (SEQ ID NO:
 45 133)

ATGGCTCCTGAAAATTTACCAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC
 CAGAGCTCCAGATCCCCCTCTTCTGGTCTTTCTGGTGCTCTATGGGCTGACCATGGCAGG
 GAACCTGGGCATCATCACCTCACCAAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT
 50 TCCTGCAACATCTGGCTCTCATTAATCTTGGTAACTCTACTGTCAATGCCCTAAAATGCTG
 ATTAACTTTTAGTAAAGAAGAAAACCTCATTCTATGAATGTGCCACCAACTGGGAG
 GGTCTTGTCTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT
 GTGGCTATTTGTAACCTCTGCTGTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGCT
 GGTCTCCCTCACATACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCATCTTATGTATTCT
 55 CTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTTACTGTGATAATGTTCTCTGTTA
 GCATTATCTTGCTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA

ATGTGGTTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGTCTATTTTA
AAAAATATGTTTCATCAGAAGGAAGGAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG
CAGTCACAAATTTTTATGGGACATTGCTATTCATGTATGTGCAGCCCCGAAGTAACCATTC
ATTGGATACTGATGATAAGATGGCTTCTGTGTTTTACACGTTGGTAATTCCTATGCTGAAT
5 CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTCATGACA
AATCTGTGCTATTCCTTTAAACAATGTAA (SEQ ID NO: 134)

AOLFR73 sequences:

10 MNHVVKHNHTAVTKVTEFILMGITDNPGLQAPLFGFLIYLVTVIGNLGMVILTYLDSKLHTP
MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFIHSELFILSAMAYDRYV
AICKPLLYVIMAEKVLWVLVIVPYLYSTFVSLFTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT
NELELILIFSGCNLLFSLIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVVIMFYGTLLFIYL
QPKSSHTLAIDKMASVFYTLIPMLNPLIYSLRNKEVKDALKRTLNRFKIPI (SEQ ID NO: 135)

15 ATGAATCATGTGGTAAAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA
TGGGGATTACAGACAACCCTGGGCTGCAGGCTCCACTGTTGGACTCTTCCTCATCATATA
TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA
CACACCCCATGTACTTTTCTTAGACATTTGTCAATCACTGATCTTGGTACTCCACTGT
CATTGCCCCGAAGATGTTAGTAACTTCATAGTGCACAAAAACACAATTTCTTACAATTGG
20 TATGCCACTCAGCTAGCATTCTTGGAGATTTTCATCATCTCTGAGCTCTTATTCTATCAGC
AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA
GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCAGTTTGTGTCACTATT
TCTCACAATTAAGTTATTTAACTGTCCTTCTGTGGCTCAAACATAATCAGCTATTTTACT
GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT
25 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT
TATTCTAGTGGCCATTCTCAGAATGAATCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC
TGTAAGTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTACTTGCA
ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCCTGTG
ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAGATGCTCTAA
30 AGAGAACTTTAACCAATCGATTCAAAATTCCCATTAA (SEQ ID NO: 136)

AOLFR74 sequences:

MEQHNLTTVNEFILTGITDIAELQAPLFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH
35 LAFMDLGYSTTVGPKMLVNFVVDKNIISYFCAATQLAFFLVFIGSELFILSAMSVDLYVAICNPL
LYTVIMSRRCQVLVAIPYLYCTFISLLVTIKFTLSFCGYNVISHFYCDLPLPLLCNTHIELI
ILIFAAIDLISLLIVLLSYLLILVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMVYQPKSSH
SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)

40 ATGGAACAACACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC
GCTGAGCTGCAGGCACCATTTATTTGCATTGTTCCCTCATGATCTATGTGATCTCAGTGATGG
GCAATTTGGGCATGATTGTCCTCACCAAGTTGGACTCCAGGTGCAAACCCCTATGTACTT
TTTTCTCAGACATCTGGCTTTCATGGATCTTGGTTATTCAACAACGTGGGACCCCAAAATG
TTAGTAAATTTGTTGTGGATAAGAATATAATTTCTTATTATTTTGTGCAACACAGCTAGC
45 TTTCTTTCTTGTGTTCAATTGGTAGTGAACCTTTTATTCTCTCAGCCATGTCCACGACCTCT
ATGTGGCCATCTGTAACCTCTGCTATACACAGTAATCATGTGCAGGAAGGTATGTCAGGT
GCTGGTAGCAATCCCTTACCTCTATTGCACATTCATTTCTTCTAGTCACCATAAAGATT
TTACCTTTGCTTTGTTCAAATACACATGAAATGAATTGATAATTGATCTTTGCAGCTAT
TGATTTGATTTCTCTCTGATAGTTCTTTTATCTTACCTGCTCATCCTTGTAGCCATTCT
50 CAGGATGAATTTCTGCTGGCAGACAAAAGGCTTTTCTACCTGTGGAGCCCAAGTCCAGTCATTCTT
GTCATAGTGTCTATGGGACTTTGCTTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCTT
TGACACTGATAAAGTGGCTTCCATATTTACACCTGGTTATCCCCATGTTGAATCCCTTGA
TCTATAGTTTACGAAACAAAGATGTAAATATGCCCTACGAAGGACATGGAATAACTTATG
TAATATTTTGTTTAA (SEQ ID NO: 138)

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AOLFR75 sequences:

MEGKNQTNISEFLLLGFSWQQQVLLFALFLCLYLTLGLFGNLLILLAIGSDHCLHTPMYFFLA
 NLSLVDLCLPSATVPKMLLNITQTQTISYPGCLAQMYFCMMFANMDNFLLTVMAYDRYVAI
 CHPLHYSTIMALRLCASLVAAPWVIAILNPLHLTLMMAHLHFCSDNVIIHFFCDINSLPLSCSD
 5 TSLNQLSVLATVGLIFVVPVCILVSYILIVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT
 GVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFIFYSLRNNELKGTLLKTLSPRGAVAHACNPSTL
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)

ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC
 10 AACACAGCAGGTGCTACTCTTTGCACTTTTCTGTGTCTCTATTTAACAGGGCTGTTTGGA
 AACTTACTCATCTTGTGCTGGCCATTGGCTCGGATCACTGCCTTCACACACCCATGTATTTCTT
 CCTTGCCAATCTGTCTTGGTAGACCTCTGCCTTCCCTCAGCCACAGTCCCCAAGATGCTAC
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCTGGCTCAGATGTATTT
 CTGTATGATGTTTGCCAATATGGACAATTTCTTCTCACAGTGATGGCATTGACCGTTAC
 15 GTGGCCATCTGTCAACCCTTACATTACTCCACATTATGGCCCTGCGCCTCTGTGCCTCTCT
 GGTAGCTGCACCTTGGGTCAATTGCACTTTTGAACCCTCTCTTGCACACTCTTATGATGGCCC
 ATCTGCACTTCTGCTCTGATAATGTTATCCACCATTCTTCTGTGATATCAACTCTCTCCTC
 CCTCTGTCTGTTCGACACACCAGTCTTAATCAGTTGAGTGTTCTGGCTACGGTGGGGCTGA
 TCTTTGTGGTACCTTCAGTGTGTATCCTGGTATCCTATATCCTCATTGTTTCTGCTGTGATG
 20 AAAGTCCCTTCTGCCAAGGAAAACTCAAGGCTTTCTCTACCTGTGGATCTCACCTTGCCCT
 GGTCACTCTTTTCTATGGAGCAAACACAGGGGTCTATATGAGCCCCCTTATCCAATCACTCT
 ACTGAAAAAGACTCAGCCGCATCAGTCATTTTATGGTTGTAGCACCTGTGTTGAATCCAT
 TCATTTACAGTTTAAGAAACAATGAAGTGAAGGGGACTTTAAAAAAGACCCTAAGCCGGC
 CGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGTGGATCA
 25 TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

AOLFR76 sequences:

MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMILILLDSHLHTPMYFFLSNLSLA
 GIGYSSAVTPKVLTGLLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY
 30 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTFRLSFCMSNVIIHFFCDKPAVITLTCSEKHISELIL
 VLISSFNVFALLVTLISYLFILITILKRHTGKGYQKPLSTCGSHLIAIFLYITVIIMYIRPSSSHSM
 DTDKIASVFYTMIPMLSPIVYTLRNKDVKNAFMKVVEKAKYSLDSVF (SEQ ID NO: 141)

ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA
 35 CTACAGGTTCCTCTTTATCATGTTTACCCTCATCTACCTCATCACTCTGACTGGGAACCT
 GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTCTCA
 GTAACCTGTCTCTTGCAGGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTAACTGG
 GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCCTGTGCTGCTCAGATGTTCTTTGT
 GCAGTCTTTGCCACTGTGGAAAATTACCTCTTGTCTCAATGGCCTATGACCGCTACGCAG
 40 CAGTGTGTAACCCCTACATTATACCACCACCATGACAACACGTGTGTGTGCTTGTCTGGC
 TATAGGCTGTTATGTCATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTTCCGC
 TCTCTTTCTGCATGTCCAATGTGATTCACTTTTTCTGTGACAAACCAGCAGTCATTACT
 CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTCTTATATCAAGTTTTAATGT
 CTTTTTGCACCTCTTGTACCTTGATTTCTATCTGTTTCATATTGATCACCATTCTTAAGAG
 45 GCACACAGGTAAGGGATACCAGAAGCCTTATCTACCTGTGGTTCTCACCTCATTGCCATT
 TTCTTATTTTATATAACTGTCATCATCATGTACATACGACCAAGTCCAGTCATTCCATGGA
 CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCCTATAGTCT
 ATACCCTGAGGAACAAAGACGTGAAGAATGCATTCAATGAAGGTTGTTGAGAAGGCAAAAT
 ATTCTCTAGATTCACTCTTTTAA (SEQ ID NO: 142)
 50

AOLFR77 sequences:

MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS
 QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFFLTMGVAEGVLLVLMSYDRYVAVC
 QPLQYPVLMRRQVCLLMGSSWVVGVLNASIQTSITLHFPYCASRVDHFFCEVPALLKLSCA
 55 DTCAYEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEEARHKAVTTCSSHITVVGLFYGA

AVFMYMVPCAYHSPQQDNVVSFLYSLVPTLNPLIYSLRNPEVWMALVKVLSRAGLRQMC
(SEQ ID NO: 143)

5 ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCTCTTCAGTCACT
CAGGATCACGCCAGCTCCTCTTCTCCCTGGTGGCTGTCATGTTTGTATAGGCCTTCTGGGC
AACACCGTTCTTCTCTTCTGATCCGTGTGGACTCCCGGCTCCACACACCATGTACTTCT
GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAGATGGCA
TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAATATTCT
TCCTCACACTGATGGGTGTGGCTGAGGGCGTCTGTTGGTCTCATGTCTTATGACCGTTA
10 TGGTGTGTGTGCCAGCCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGCTG
ATGATGGGCTCCTCCTGGGTGGTAGGTGTGCTCAACGCCTCCATCCAGACCTCCATCACC
TGCATTTTCCCTACTGTGCTCCCGTATTGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA
CTGAAGCTCTCCTGTGCAGATACCTGTGCTACGAGATGGCGCTGTCCACCTCAGGGGTGC
TGATCCTAATGCTCCCTCTTCCCTCATCGCCACCTCCTACGGCCACGTGTTGCAGGCTGT
15 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGTGTACCATCTGCTCCTCGCACATCA
CGGTAGTGGGGCTCTTTATGGTGGCGCCGTGTTTATGTACATGGTGCCTTGGCGCTACCA
CAGTCCACAGCAGGATAACGTGGTTTCCCTCTTCTATAGCCTTGTACCCCTACACTCAAC
CCCCTTATCTACAGTCTGAGGAATCCGGAGGTGTGGATGGCTTGGTCAAAGTGCTTAGCA
GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

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AOLFR78 sequences:

MSPDGNHSSDPTEFVLAGLPNLNSARVELFSVLLVYLLNLGNVLIVGVVRADTRLQTPMYF
FLGNLSCLEILLTSVIIPKMLSNFLSRQHTISFAACITQFYFYFFLGASEFLLAVMSADRYLAICH
PLRYPLMSGAVCFRVALACWVGGGLVPVLPVAVALLPFCKQGAUVVQHFFCDSPGLRLAC
25 TNTKKLEETDFVLASLVVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVTLFYGSAI
FLYVRPSQSGSVDTNWAVTVITTFVTPLLNPFYALRNEQVKEALKDMFRKVAVGLGNLLD
KCLSEKAVK (SEQ ID NO: 145)

30 ATGAGTCCTGATGGGAACCACAGTAGTGATCCAACAGAGTTCGTCTTGGCAGGGCTCCCA
AATCTCAACAGCGCAAGAGTGGAATTATTTCTGTGTTTCTTCTGTCTATCTCCTGAATCT
GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACAGACCCCTAT
GTACTTCTTTCTGGGTAACTGTCTGCTAGAGATACTGCTCACTTCTGTATCATTTCCAA
AGATGCTGAGCAATTTCTCTCAAGGCAACACACTATTTCTTTGCTGCTATCATCCCCA
ATTCTATTTCTACTTCTTCTCGGGGCTCCGAGTTCTTACTGTTGGCTGTCTGTGCGG
35 ATCGCTACCTGGCCATCTGTCTCCTCTGCGCTACCCCTTGTCTGATGAGTGGGGCTGTGTG
CTTTCGTGTGGCCTTGGCCTGCTGGGTGGGGGACTCGTCCCTGTGCTTGGTCCCACAGTG
GCTGTGGCCTTGCTTCTTTCTGTAAGCAGGGTGCTGTGTACAGCACTTCTTCTGCGACA
GTGGCCCACTGCTCCGCTGGCTTGCACCAACACCAAGAAGCTGGAGGAGACTGACTTTGT
CCTGGCCTCCCTCGTCATTGTATCTTCTTGTGATCACTGCTGTGCTTACGGCCTCATTG
40 TGCTGGCAGTCTGAGCATCCCTCTGCTTCAAGGCGTCAGAAGGCTTCTTACCTGTAC
CTCCCACTTGATAGTGGTGACCCTCTTCTATGGAAGTGCCATTTTCTCTATGTGCGGCCAT
CGCAGAGTGGTTCTGTGGACACTAACTGGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
CACTGTTGAATCCATTCTATGCCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA
CATGTTTAGGAAGGTAGTGGCAGGCGTTTTAGGGAATCTTTTACTTGATAAATGTCTCAGT
45 GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

AOLFR79 sequences:

MTPGELALASGNHTPVTKFILOQFSNYPDLQELLFGAILLIYAIVVGNLGMALIFTDSHLQSP
MYFFLNVLVSFLDICYSSVVPKLLVNFLVSDKSISFEGCVVQLAFFVHVTAESFLLASMAFYDR
50 FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANSAIQTNVFPALFCGPNQLTHYCDIPPLH
LACANTATARVVLVYFVSALVTLPAAVILTSYCLVLVAIGRMRSVAGREKDLSTCASHFLAIAI
FYGTVVFTYVQPHGSTNNTNGQVVSFYTIIIPMLNPFYSLRNKEVKALQRLQVNIFFG
(SEQ ID NO: 147)

55 ATGACACCTGGAGAACTAGCCCTTGCCAGTGGCAACCACACCCCAAGTCAACCAAGTTCATCT
TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTTCTTCTCGGAGCCATCCTGCTCAT

CTATGCCATAACAGTGGTGGGCAACTTGGGAATGATGGCACTCATCTTCACAGACTCCCAT
 CTCCAAAGCCCAATGTATTTCTTCTCAATGTCCTCTCGTTTCTTGATATTTGTTACTCTTCT
 GTGGTCACACCTAAGCTCTTGGTCAACTTCTGGTCTCTGACAAGTCCATCTCTTTTGAGG
 GCTGTGTGGTCCAGCTCGCCTTCTTTGTAGTGCATGTGACAGCTGAGAGCTTCTGCTGGC
 5 CTCCATGGCCTATGACCGCTTCTAGCCATCTGTCAACCCCTCCATTATGGTTCTATCATGA
 CCAGGGGGACCTGTCTCCAGCTGGTAGCTGTGTCTATGCATTTGGTGGAGCCAACTCCGC
 TATCCAGACTGGAAATGTCTTTGCCCTGCCTTTCTGTGGGCCCCAACAGCTAACACACTAC
 TACTGTGACATAACACCCCTTCTCCACCTGGCTTGTGCCAACACAGCCACAGCAAGAGTGG
 TCCTCTATGTCTTTCTGCTCTGGTCACCTTCTGCCTGCTGCAGTCATTCTCACCTCCTACT
 10 GCTTGGTCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT
 CCACTTGTGCCTCCCACTTTCTGGCCATTGCCATTTTCTATGGCACTGTGGTTTTACCTAT
 GTTCAGCCCCATGGATCTACTAACAAATACCAATGGCCAAGTAGTGCCGTCTTCTACACCA
 TCATAATTCCCATGCTCAATCCCTTCTATAGCCTCCGCAACAAGGAGGTGAAGGGCGC
 TCTGCAGAGGAAGCTTCAGGTCAACATCTTTCCCGGCTGA (SEQ ID NO: 148)

15

AOLFR80 sequences:

MEGINKTAKMQFFRPFSPDPEVQMLIFVFLMMYLTSLGGNATIAVIVQINHSLHTPMYFFLA
 NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFFVFLGGADCVLLVVMAYDRFIAICH
 PLRYRLMSWSLCVELLVGSLVLGFLLSLPLTILIFHLPFCHNDEIYHFYCDMPAVMRLACADTR
 20 VHKTALYIISFIVLSIPLSLISISYVFIVVAILRIRSAEGRQAYSTCSSHLVLLQYGCTSFYILSPS
 SSYSPEMGRVVSVA YTFITPILNPLIYSLRNKELKDALRKALRK (SEQ ID NO: 149)

ATGGAAGGAATAAATAAACTGCAAAGATGCAGTTTTTCTTTCGTCCATTCTCACCTGACC
 CTGAGGTCCAGATGCTGATTTTTGTGGTCTTCTGATGATGTATCTGACCAGCCTCGGTGG
 25 AAATGCTACAATTGCAGTCATTGTTGATCAATCATTCCCTCCACACCCCATGTACTTTT
 TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCCATGGCCTTG
 GCAAACCTCCTTTCAATGGGCAAACTCCTGTTTCCATCACGGGATGTGGCAGCCAGATGT
 TTTCTTTGTCTTCTGGGTGGGGCTGATTGTGTCTGCTGGTAGTCATGGCTTATGACCGG
 TTTATAGCGATCTGTACCCCTCTGCGATACAGGCTCATCATGAGCTGGTCTTGTGTGTGG
 30 AGCTGCTGGTAGGCTCCTTGGTGTGGGGTCTGTTGTCACTGCCACTCACCATTTTAATC
 TTCCATCTCCCATTTCTGCCACAATGATGAGATCTACCATTCTACTGTGACATGCCTGCAGT
 CATGCGCCTGGCTTGTGCAGACACACGCGTTCACAAGACTGCTCTGTATATCATCAGCTTC
 ATCGTCCTTAGCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTGGTAGCCAT
 TTTACGGATCCGGTCAGCAGAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC
 35 TTAGTGGTCTCCTGCAGTATGGCTGCACCAGCTTTATATACTTGTCCCCCAGTCCAGCTA
 CTCTCCTGAGATGGGCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC
 CCCTTGATCTATAGTTTGAGGAACAAGGAAGTAAAGATGCCCTAAGGAAAGCATTGAGA
 AAATTCTAG (SEQ ID NO: 150)

40 **AOLFR81 sequences:**

MGVKNHSTVTEFLLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS
 LSFLDFCYSSVITPKMMKLWMESHLIVPETRPSRPMMSNQLVTEFILQGFSEHPEYRVFLSCF
 LFLYSGALTGNVLITLITFNPGLHAPMYFFLLNLATMDICTSSIMPKALASLVSEESSISYGGC
 MAQLYFLTWAASSELLLLTVMAYDRYAAICHPLHYSSMMSKVFCGLATAVWLLCAVNTAIH
 45 TGLMLRLDFCGPNVIIHFFCEVPPLLLSCSSTYVNGVMIVLADAFYGIVNFMITIASYGFIVSSI
 LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSYSAGSKLAGLLYTVLSPTLNPL
 IYTLRNKEVKAAALRKLPFFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCCAGAAACCCGTCCCAGCCCAAGGATG
 50 ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGCACCCAGAAT
 ACCGGGTGTTCTTATTACAGCTGTTTCTTCTCTACTCTGGGGCCCTCACAGGTAATGTC
 CTCATACCTTGGCCATCACGTTCAACCCTGGGCTCCACGCTCCTATGTACTTTTTCTTACT
 CAACTTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCCAAGGCGCTGGCCAGT
 CTGGTGTGGAAGAGAGCTCCATCTCCTACGGGGGCTGCATGGCCAGCTCTATTTCTCA
 55 CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTCATGGCCTATGACCGGTACGCAGC
 CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC

WO 01/98526

ACAGCCGTGTGGCTGCTCTGCGCCGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT
 TGGATTTCTGTGGCCCAATGTCATTATCCATTCTTCTGCGAGGTCCCTCCCCTGCTGCTT
 CTCTCCTGCAGCTCCACCTACGTCAACGGTGTCTATGATTGTCTGCGGATGCTTTCTACG
 GCATAGTGAACCTCCTGATGACCATCGCGTCTATGGCTTCATCGTCTCCAGCATCCTGAA
 5 GGTGAAGACTGCCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTTCCCACCTACCGTG
 GTGTGCATGTATTACACCGCTGTCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG
 CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGCTGAGTCTACCTCAACCCCTT
 CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTCCCTTTCTTC
 AGAAATTAA (SEQ ID NO: 152)

10

AOLFR82 sequences:

MQLNNNVTEFILLGLTQDPFWKKIVFVIFLRLYLGTLLGNLLIISVKASQALKNPMFFFLFYLSL
 SDTCLSTSIAPRMIVDALLKTTISFSECMQVFSSHVFGLEIFILITAVDRYVDICKPLHYMTII
 SQWVCGVLMMAVAVWGSCVHSLVQIFLALSFPFCGPNVINHCDFDLQPLLKQACSETYVNNLL
 15 VNSGAICAVSYVMLIFSIVIFLHSLRNHSAEVIKKALSTCVSHIIVILFFGPCIFMYTTPATVFP
 MDKMIAVFYTVGTSFLNPVIYTLKNTEVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

20

ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT
 GGAAGAAAATAGTGTGTTGTTATTTTTTTCGCTCTCTACTTGGGAACACTGTTGGGTAATTT
 GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACTTAAGAACCCAATGTTCTTCTTCCTT
 TTCTACTTATCTTATCTGATACTTGCCTCTCTACTTCCATAGCCCTAGAAATGATTGTGGA
 TGCCCTTTTGAAGAAGACAACATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC
 CATGTCTTTGGCTGCCTGGAGATCTTCATCCTCATCCTCAGCGGTGTGACCGCTATGTGGA
 CATCTGTAAGCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTGTTGATG
 25 GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTTCTTGCCTGAGTTT
 GCCATTCTGTGGCCCAATGTGATCAATCACTGTTTCTGTGACTTGACGCCCTTGTGAAA
 CAAGCCTGTTTCAGAAACCTATGTGGTTAACTACTCCTGTTTCCAATAGTGGGGCCATTT
 GTGCAGTGAAGTTATGTGCTAATATTCTCCTATGTCTCTTCTGCACTCTCTGAGAAAC
 CACAGTGTGAAGTGATAAAGAAAGCACTTTCCACATGTGTCTCCACATCATTGTGGTCA
 30 TCTTGTCTTTGGACCTTGCATATTTATGTACACATGCCCTGCAACCGTATTCCCCATGGAT
 AAGATGATAGCTGTATTTTATACAGTTGGAACATCTTTCTCAACCCTGTGATTTACACGCT
 GAAGAATACAGAAGTGAAGAGTCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGA
 TGACAAAAGATAA (SEQ ID NO: 154)

35 **AOLFR83 sequences:**

MGNWTAAVTEFVLLGFSLSREVELLLLVLPTFLLTLLGNLLIISTVLSCSRHTPMYFFLCNL
 SILDILFTSVISPKVLANLGSRDKTISFAGCITQCYFYFFLGTVEFLLLTVMYSYDRYATICPLRYT
 TIMRPSVCIGTVVFSWVGFLSVLFPTILISQLPFCGSNIINHFFCDSDGPLLALACADTTAIELMDF
 MLSSMVLCCIVLVAYSYTYIILTIVRIPSASGRKKAFNTCASHLTIVIPSGITVFIYVTPSQKEYL
 40 EINKIPLVLSSVTPFLNPFIYTLRNDTVQGVLRDVWVRVGVFEKRMRAVLSRLSSNKDHQ
 GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

45

ATGGGTAACTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG
 AGGTGGAGCTGCTGCTCCTGGTCTCTGCTGCCACGTTCTGCTGACTCTTCTGGGGAA
 CCTGCTCATCATCTCCACTGTGCTGCTGCTCCCGCTCCACACCCCATGACTTCTTCT
 TGTGCAACCTCTCTATCCTGGACATCCTCTTCACTCAGTCATCTCTCCAAAAGTGTGGCC
 AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCAGTGCTATTCT
 ACTTTTTCTTGGGCACAGTTGAGTTCTCCTGCTGACGGTCATGTCCTATGACCGTTATGCC
 ACCATCTGCTGCCCCCTGCGGTACACCACCATCATGAGACCTTCTGTCTGCAATTGGGACCG
 50 TTGATTCTCTTGGGTGGGAGGCTTCTGTCTGTGCTCTTTCCAACCATCCTCATCTCCAG
 CTGCCCTTCTGTGGCTCCAATATCATTAAACCACTTCTTCTGTGACAGTGGACCTTGTGGC
 CCTGGCCTGTGCAGACACCACTGCCATCGAGCTGATGGATTTTATGCTTTCTTCCATGGTC
 ATCCTCTGCTGCATAGTCTCGTGGCCTATTCTATACGTACATCATCTTGACCATAGTGCG
 CATTCCTTCTGCAAGTGAAGGAAGAAGGCCTTTAATACCTGTGCTTCCACCTGACCATA
 55 GTCATCATTCTAGTGGCATCACTGTGTTTATCTATGTGACTCCCTCCAGAAAGAATATCT
 GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGAAGTCCATCCTCAACCCCTT

ATATATACTCTGAGGAATGACACAGTGCAGGGAGTCCTCAGGGATGTGTGGGTCAGGGTT
CGAGGAGTTTTTGAAGAGGATGAGGGCAGTGCTGAGAAGCAGATTATCCTCCAACAAA
GACCACCAAGGAAGGGCTTGCTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGTT
AG (SEQ ID NO: 156)

5

AOLFR85 sequences:

MGAKNNVTEFVLFGLFESREMQHTCFVVFVFLHVLTVLGNLLVIITINARKTLKSPMYFFLSQL
SFADICYPSTTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY
TAIMDCRKCGLLAGASWLAGFLHSILQTLTVQLPFCGPNEIDNFFCDVHPLLKLACADTYMV
10 GLIVVANSGLMISLASFILIIISYVILLNLRSSQSEDRRKAVSTCGSHVITVLLVLMPPMFMYIRPS
TTLAADKLIILFNIVMPPLNPLIYTLRNNDVKAMRKLFRVKRSLGEK (SEQ ID NO: 157)

ATGGGTGCCAAGAACAATGTGACTGAGTTTGTATTTTGGCCTTTTTGAGAGCAGAGAGA
TGCAGCATACATGCTTTGTGGTATTCTTCTCTTTCATGTGCTCACTGTCCTGGGGAACCTT
15 CTGGTCATCATCACCATCAATGCTAGAAAGACCCTGAAGTCTCCCATGTATTTCTTCTCTGA
GCCAGTTGTCTTTTGCTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGAC
ACTTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTTCTGCCCA
CTTCTTTGGTGGCACTGAGATCTTCTCCTTACAGCCATGGCCTATGACCGCTATGTGGCC
ATCTGTAGGCCCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG
20 GGGCCTCCTGGTTAGCTGGCTTCTGCAATCCATCCTGCAGACCCTCCTCACGGTTCAGCTG
CCTTTTGTGGGCCCAATGAGATAGACAACTTCTTCTGTGATGTTTCATCCCCTGCTCAAGTT
GGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTTCT
TTAGCATCCTTTTTATCCTTATCATTTCCTATGTTATCATCTTACTGAACCTAAGAAGCCA
GTCATCTGAGGACCGGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCCTT
25 TTGGTTCTCATGCCCCCATGTTTCATGTACATTTCGTCCTCCACCACCCTGGCTGCTGACAA
ACTTATCATCCTCTTTAACATTGTGATGCCACCTTTGCTGAACCCTTTGATCTATACACTAA
GGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG
AGAAGTGA (SEQ ID NO: 158)

30 **AOLFR86 sequences:**

MQLVLLLMFLLVFIGNTAPAFSVTLESMDIPQNITEFFMLGLSQNSEVQRVLFVVFLLIYVVTVC
GNMLIVVTITSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHF
LGGVEIILLTVMAYDRYVAICKPLHNTTIMTRHLCAMLVGVAWLGGFLHSLVQLLLVLWLPFC
GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFLMLAASYVILYSLRSHSADGRC
35 KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR
KLFTW (SEQ ID NO: 159)

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT
CTCAGTGACCTTGGAAATCTATGGACATAACCACAAAATATCACAGAATTTTTTCATGCTGGGG
40 CTCTCACAGAACTCAGAGGTACAGAGAGTTCTCTTTGTGGTCTTTTGTGCTGATCTATGTGG
TCACGGTTTGTGGCAACATGCTCATTGTGGTCACTATCACCTCCAGCCCCACGCTGGCTTC
CCCTGTGTATTTTTCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTTCTTCTATGGC
TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG
GCTCAGCTCTTTGGAGCTCATTTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG
45 CTTATGACCGCTATGTGGCCATCTGTAAGCCCCTGCACAATACTACCATCATGACCAGGCA
TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCTGCTCATTGCTGCTGCTG
CTCCTCCTGGTCTTTGGTTGCCCTTCTGTGGGCCCAATGTGATCAATCACTTTGCTGTGA
CTTGTAACCTTTGCTGGAAGTTGCCTGCACCAATACGTATGTCATTGGTCTGCTGGTGGTT
GCCAACAGTGGTTAATCTGCCTGTTGAACCTCCTCATGCTGGCTGCCTCCTACATTGTCAT
50 CCTGTACTCCTTGAGGTCCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA
GCCCACTTCATTGTTGTTGCCCTGTTCTTTGTGCCCTGTATTTTACTTATGTGCATCCATTT
TCTACTTTACCTATAGACAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA
TCCACTCATTTATACCCTGAGAAATGAAGAGGTAAAAAATGCCATGAGAAAGCTCTTTACA
TGGTAA (SEQ ID NO: 160)

55

AOLFR87 sequences:

MNNIAQLSLGFIDLGPSVLQKIILTKIILLFKMYVSNCPCAIHRKINYPNTKLDFEQVNNITEFI
 LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLIVVTITSPALDSPVYFFLSFFSFIDGCSSTMAP
 KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILLVVMAYDCYVAICKPLYLITMNRQVCGL
 5 LVAMAWVGGLHALIQMLLIVWLPFCGPNVIDHFICDLFLLKLSCTDTHVFGLFVAANSGLM
 CMLIFSILITSYVLILCSQRKALSTCAFHITVVVLFVPCILVYLRPMITFPIDKAVSVFYTVVTPM
 LNPLIYTLRNTVEKNAMKQLWSQIHWGNLCD (SEQ ID NO: 161)

10 ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC
 AGAAAATAATCCTGACCAAAATTATTTTATTGTTCAAAATGTATGTGTCAAATTGCAATCC
 TTGTGCTATTACAGAAAAATCAATTATCCAAATACAAACTGGATTTCGAGCAAGTGAAC
 AACATAACGGAATTCATCTTGCTTGGCCTGACACAGAACGCAGAGGCACAGAACTCTTGT
 TTGCTGTGTTTACACTCATCTACTTTCTCACCATGGTAGACAACCTAATCATTGTGGTGACA
 15 ATCACCACCAGCCCAGCCCTGGACTCCCCCGTGATTTTTTTCTGTCTTTCTTTCTCTCAT
 AGATGGCTGCTCCTCTTCTACCATGGCCCCCAAAATGATATTTGACTTACTCACTGAAAAG
 AAAACTATTTCTTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTTCTTTGGGGAG
 TTGAGATCATTCTGCTCGTGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCCT
 GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTG
 GGGGGATTTCTTCACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTCTGTGGCCC
 20 CAATGTCAATTGACCATTTTCATCTGTGACCTTTTCCCTCTGCTAAAACTCTCCTGCACTGACA
 CTCACGTCTTTGGACTCTTTGTTGCCGCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT
 ATTCTTATTACCTCTTACGTCCTAATCCTCTGCTCACAGCGGAAGGCTCTCTACCTGCGC
 CTTCCATATCACTGTAGTCGTCCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA
 TGATCACCTCCCTATTGATAAAGCTGTGTCTGTGTTTTATACTGTGGTAACCCCATGTGA
 25 AACCCTTTAATCTACACCCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG
 AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

AOLFR88 sequences:

30 MWQKNQTSADFILEGLFDDSLTHLFLSLTMVVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ
 LSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYLCLGGAECFLAVMSYDRYVAICH
 PLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHFPFCGPRKVYHFYCEFAVVKLVC
 GDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSKRNAFATCGSHLTVVSLWFGACIFS
 YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNDVAKALRRVLRRDVITQCIQRLQLWLP
 RV (SEQ ID NO: 163)

35 ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT
 CCCTTACCCACCTTTTCTCTCTTGACCATGGTGGTCTTCCTTATTGCGGTGAGTGGC
 AACACCCCTACCAATTCTCCTCATCTGCATTGATCCCCAGCTTCATACACCAATGTATTTCT
 40 GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT
 ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTC
 TCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCTATGACCGCTAT
 GTTGCCATCTGTCTCATCCACTGCGCTATGCTGTGCTCATGAACAAGAAGGTGGGACTGATGA
 TGGCTGTCTGTCTATGGTTGGGGGCATCCGTGAACCTCCCTAATTCACATGGCGATCTTGAT
 GCACTTCCCTTTCTGTGGGCTCGGAAAGTCTACCACTTCTACTGTGAGTTCCCAGCTGTTG
 45 TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATTCT
 CCTCCTCCTCCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTTCAAAGTGTCAATCA
 GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTGTGGCTCCCACCTCAGGGTG
 GTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGGTCCCAGTGCATCT
 ATTGCAGAACAAAGTGGTCTGTGTTCTACAGCATCATTACGCCACATTGAATTCTCTG
 50 ATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGTGAGGAGAGAT
 GTTATACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTGTAG (SEQ ID NO:
 164)

AOLFR89 sequences:

55 MLDPSISSHTLYLHSLFPQGLRKGTMWQKNQTSADFILEGLFDDSLTHLFLSLTMVVFLIAVS
 GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYL

CLGGAECFLLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHF
PFCGPRKVYHFYCEFPVVKLVCGDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSK
RNAFATCGSHLTVVSLWFGACISYMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA
KALRRVLRDVTQCIQRLQLWLPRV (SEQ ID NO: 165)

5

ATGCTGGACCCAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT
GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG
GCTCTTCGATGACTCCCTTACCCACCTTTTCCTTTTCTCCTTGACCATGGTGGTCTTCCTTAT
TGCGGTGAGTGGCAACACCCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACA
10 CCAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT
CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA
ACCCAGCACTTCCTCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCATGTC
CTATGACCGCTATGTTGCCATCTGTCATCCACTGCGCTATGCTGTGCTCATGAACAAGAAG
GTGGGACTGATGATGGCTGTCATGTCATGGTTGGGGGCATCCGTGAACCTCCCTAATTCACA
15 TGGCGATCTTGATGCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCATTCTACTGTGA
GTTCCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC
ATCAGCAGCATTCTCCTCCTCCTCCCCATCTTCCTGATTCTACATCCTATGTCTTCATCCTT
CAAAGTGTCAATCAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTGTGGCT
CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGG
20 TCCCAGTGCACCTCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCA
CATTGAATTCTCTGATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT
GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTG
TAG (SEQ ID NO: 166)

25 AOLFR90 sequences:

MFSMTTEALNNFALGCTNLLMTMPIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQNPVQEIVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINS
30 FICIINFSLLLVSAYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 167)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACCTGGATGTACCAACTTGTTAA
TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCCTTTGTCCTAATTGCAGACTATA
35 CATGATCCCTGTTGGAGCTTTTCATCTTTTCCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCCTGCTGGGACTTTCACAGAATCCAAATGTTTCAGGAAATAGTATTTGTTG
TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTTCTC
AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCTTCTGGA
TGCCTGCTTCTCATCTGTCATCACCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
40 ACCATCTCTTTTGAAGGCTGCATGATGACGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCTCAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
GGCCTCTTGCAATCCATGATACAAATTCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
45 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTCTTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
TATTTGTATATACACGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC
50 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAATATTA
AACTTTAA (SEQ ID NO: 168)

AOLFR91 sequences:

MGNWSTVTEITLIAFPALLEIRISLFVVLVVTYTLTATGNITHSLIWIDHRLQTPMYFFLSNLSFL
55 DILYTTVITPKLLACLLGEEKTISFAGCMIQTYFYFFLGTVEFILLAVMSFDRYMAICDPLHYTVI
MNSRACLLLVLCWVGAFSLVLFPTIVVTRLPCYRKEINHFFCDIAPLLQVACINTHLIEKINFL

SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD
YDKVA AVLITVVTPLNPFYISLRNEKVQEVLRQETVNRIMTLIQRKT (SEQ ID NO: 169)

5 ATGGGAAACTGGAGCACTGTGACTGAAATCACCTAATTGCCTTCCCAGCTCTCCTGGAGA
TTCGAATATCTCTCTTCGTGGTTCTTGTGGTAACTTACACATTAACAGCAACAGGAAACAT
CACCATCATCTCCCTGATATGGATTGATCATCGCCTGCAAACTCCAATGTACTTCTTCTCA
GTAATTTGTCTTTCTGGATATCTTATACCACTGTCATTACCCCAAAGTTGTTGGCCTGC
CTCCTAGGAGAAGAGAAAACCATATCTTTGCTGGTGCATGATCCAAACATATTTCTACT
TCTTTCTGGGGACGGTGGAGTTTATCCTCTTGGCGGTGATGTCCTTTGACCGCTACATGGC
10 TATCTGCGACCCACTGCACTACCGTGCATCATGAACAGCAGGGCCTGCCTTCTGCTGGT
CTGGGATGCTGGGTGGGAGCCTTCTGTCTGTGTTGTTTCCAACCATTGTAGTGACAAGGC
TACCTTACTGTAGGAAAGAAATTAATCATTCTTCTGTGACATTGCCCTCTTCTTCAGGTG
GCCTGTATAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTGTGCATCCT
GAGCTCCCTGGCATTCACTACTGGGTCTACGTGTACATAATTTCTACCATCCTGCGTATCC
15 CCTCCACCCAGGGCCGTCAGAAAGCTTTTTCTACCTGTGCTTCTCACATCACTGTTGTCTCC
ATTGCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT
ATGACAAGGTGGCCGCTGTCTCATCAGTGGTGACCCCTCTCCTGAACCTTTTATCTA
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTGAGAGAGACAGTGAACAGAATCATGAC
CTTGATACAAAGGAAAACCTGA (SEQ ID NO: 170)

20

AOLFR92 sequences:

MRNGTVITEFILLGFPVIQGLQTPLFIAIFLYILTLAGNGLIATVWAEPLQIPMYFFLCNLSFLE
IWYTTTVPKLLGTFVARTVICMSCCLLQAFHFFVGTTEFLILTIMSFDRLTICNPLHPTIM
TSKLCLQALSSWVVGFTIVFCQTMILLIQLPCGNNVISHFYCDVGPSLKAACIDTSILELLGVIA
25 TILVIPGSLLFNMISYIYILSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK
INKVSVLNTILTPLLNPFIYTIRNKEVKGALRKAMTCPKTGHAH (SEQ ID NO: 171)

30 ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCTGTTATCCAAGGCC
TACAAACACCTCTCTTTATTGCAATCTTTCTCACCTACATATTAACCCTTGAGGCAATGGG
CTTATTATTGCCACTGTGTGGGTGAGCCAGGCTACAAATCCAATGTACTTCTTCTCTTGT
TAACTTGTCTTTCTAGAAATCTGGTACACCACCACAGTCATCCCCAACTGCTAGGAACC
TTTGTAGTGGCAAGAACAGTAATCTGCATGTCCTGCTGCCTGCTGAGGCCCTTCTTCACT
TCTTCGTGGGCACCCAGGTCTTGATCCTCACTATCATGTCTTTTGACCGCTACCTCACC
ATCTGCAATCCCCCTTACCACCCCACTCATGACCAGCAAACTCTGCCTGCAGCTGGCCC
35 TGAGCTCCTGGGTGGGCTTACCATTGTCTTTGTGACGATGCTGCTCATCCAGTT
GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCCAGTTTGAAA
GCCGCTGCATAGACACCAGCATTTTGGAACTCCTGGGCGTCATAGCAACCATCCTTGTGA
TCCAGGGTCACTTCTCTTTAATATGATTTCTTATCTACATTCTGTCCGCAATCCTACGA
ATTCCTTCAGCCACTGGCCACCAAAAGACTTTCTACCTGTGCCTCGCACCTGACAGTTGT
40 CTCCTGTCTACGGGGCTGTCTGTTCATGTACCTAAGACCCACAGCACTCCTCCTTTA
AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCTTCTGAATCCCTTTATT
TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCAAG
ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

45 **AOLFR93 sequences:**

MLMNYSSATEFYLLGFPGSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGHL
SALEILVTIIVPVMWLWLLLPQMOTIYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN
PLRYNIIMNRHTCNFVVLVSUVFGFLFQIWPVYVMFQLTYCKSNVNNFFCDRGQLKLSCN
NTLTFEFILFLMAVFVLFGLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCLFLY
50 VKPKQTQAADYNWVSLMVSVVTPLNPFIFTLRNDKVIEALRDGVKRCCLFRN (SEQ ID
NO: 173)

55 ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA
ACTACATCATATCCTTTTTGCTATATTCTCTTTTCTACTTGGTGACATTAATGGGAAACA
CAGTCATCATCATGATTGTCTGTGTGATAAACGTCTGCAGTCCCCATGATTTCTTCTCCT
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAACCATAATCGTCCCGTGATGCTTTGGG

GATTGCTGCTCCCTGGGATGCAGACAATATATTGTCTGCCTGTGTTGTCCAGCTCTTCTTG
 TACCTTGCTGTGGGGACAACAGAGTTCGCATTACTTGGAGCAATGGCTGTGGACCGTTATG
 TGGCTGTCTGTAACCCCTCTGAGGTACAACATCATTATGAACAGACACCTGCAACTTTGT
 5 GGTTCTTGTGTCATGGGTGTTTGGGTTCTTTTCAAATCTGGCCGGTCTATGTCATGTTTC
 AGCTTACTTACTGCAAATCAAATGTGGTGAACAATTTTTTTGTGACCGAGGGCAATTGCT
 CAAACTATCCTGCAATAATACTCTTTTACGGAGTTTATCCTCTTCTTAATGGCTGTTTTG
 TTCTCTTGGTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATCTC
 AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACCTG
 10 TGTGTGATTGGCTACGGCAGCTGCTTGTCTCTACGTGAAACCCAAAGCAACGCAGGCA
 GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTCAGTAGTAACCTCTTCTCAATCCTTT
 CATCTTACCCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC
 TGTCAACTATTCAGGAATTAG (SEQ ID NO: 174)

AOLFR94 sequences:

15 METWVNQSYTDGFFLLGIFSHSTADLVLFVVMVAVFTVALCGNVLLIFLIYMDPHLHTPMYFF
 LSQSLMDLMLVCTNVPKMAANFLSGRKSISFVCGIQIGLVCLVVGSEGLLLGLMAYDRYVA
 ISHPLHYPILMNQRVCLQITGSSWAFGIIDGLIQMVVMNFPYCGLRVNHFCEMLSLLKLAC
 VDTSLFEKVIFACCVFMLLPFSIIVASYAHILGTVLQMHSAQAWKKALATCSSHLTAVTLFYG
 20 AAMFIYLRPRHYRAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH
 (SEQ ID NO: 175)

ATGGAGACGTGGGTGAACCAGTCTACACAGATGGCTTCTTCTCTTAGGCATCTTCTCCC
 ACAGTACTGCTGACCTTGTCTCTTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT
 25 GGAATGTCTCTCATCTTCTCATCTACATGGACCTCACCTTCACACCCCATGTACTT
 CTTCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG
 GCAGCCAACTTCTGTCTGGCAGGAAGTCCATCTCCTTTGTGGGCTGTGGCATAAAATTG
 GCCTCTTGTCTGTCTTGTGGGATCTGAGGGGCTTGTCTGGGACTCATGGCTTATGACCG
 CTATGTGGCCATTAGCCACCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC
 AGATTACTGGGAGCTCCTGGGCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT
 30 AATGAATTTCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCC
 TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTTGCTTGTGTG
 TCTTCATGCTTCTTCCATTCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT
 GTGCTGCAAAATGCACTCTGCTCAGGCCTGGAAAAAGGCCCTGGCCACCTGCTCTCCACC
 TGACAGCTGTCAACCTCTTCTATGGGGCAGCCATGTTCTATCTACCTGAGGCCTAGGCACTA
 35 CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCTTACTCCCATGCTC
 AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG
 GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

AOLFR95 sequences:

40 MLGSKPRVHLIYLPASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLVYAMILL
 GNVGMMTHMTDPRLNTPMYFFLGNLSFIDLFYSSVIEPKAMINFWSENKSISFAGCVAQLFLFA
 LLIVTEGFLLAAMAYDRFLAICNPLLYSVQMSTRCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS
 RAVDHFYCDSPQLRSLCSDFIHRMISFSLSCIILPTHVIIVSVMYIVSTVLKIHSTEGHKKAFST
 45 CSSHLGVSVLYGAVFFMYLTPDRFPELSKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLE
 KKNIL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCAATTTGTATATTTTGCCTGTGCCTCTCAACAGGTTTC
 TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCACTTCTGCAGG
 50 CTTCAGGGTACGCCAGAGCTCCACATTCTCCTCTCCTGCTATTTTGTGTTTATGCCA
 TGATCCTTCTAGGGAATGTTGGGATGATGACCAATTATTATGACTGATCCTCGGCTGAACAC
 ACCAATGATTTTTCTAGGCAATCTCTCCTTCATTGATCTTTTCTATTCTGTTATTGA
 ACCAAGGCTATGATCAACTCTGGTCTGAAAAACAAGTCTATCTCCTTTGCAGGCTGTGTG
 GCCCAGCTCTTCTCTTTGCCCTCCTCATTTGACTGAGGGATTTCTCCTGGCGCCATGGC
 TTATGACCGCTTATTTGCCATCTGCAACCCCTGCTCTACTCTGTTCAAAATGTCCACAGTC
 55 TGTGTACTCAGTTGGTGGCTGGTTCCTATTTTGTGGCTGCATTAGCTCAGTTATTCAGACT
 AGCATGACATTTACTTTATCTTTTTCGCTTCTCGGGCTGTTGACCACTTTTACTGTGATTC

WO 01/98526

TCGCCCCACTTCAGAGACTGTCTTGTTCTGATCTCTTTATCCATAGAATGATATCTTTTTCCT
 TATCATGTATTATTATCTTGCCTACTATCATAGTCATTATAGTATCTTACATGTATATTGTG
 TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT
 CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGTCTTTTTTATGTATCTCACTCCTGAC
 5 AGATTTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA
 ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAATTTCTAGA
 GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

AOLFR96 sequences:

10 MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAIYTVTLLGNFLIVTVTSVDLALQTPMYFFLQN
 LSLLEVCFLLVMVPKMLVDLVSPRKIISFVCGTQMYFFFFFGSSECFLLSMAYDRFVAICNP
 LHYSVIMNRSCLLWMAIGSWMSGVPVSMQLTAWMMALPFCGPNAVDFHFFCDGPPVLKLVTV
 DTTMYEMQALASTLLFIMFPFCLILVSYTRIHTILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL
 TYLRPKSNQSPESKKLVLSYTVITPMLNPIIYGLRNNEVKGAVKRTITQKVLQKLDVF (SEQ
 15 ID NO: 179)

ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC
 CCGAGATGCAAGTTTCCCTCTTATTTTTTCTGGCCATTTATACAGTCACTTTGTGGGC
 AACTTTCTTATTGTACAGTTACCAGTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT
 20 TCTTCAAAATCTGTCACTTCTTGAAGTATGTTTACCTTGGTTATGGTGCCAAAAATGCTTG
 TAGATCTAGTGTCCCAAGGAAATATCTCTTTTGTGGGCTGTGGTACCCAGATGTACTT
 CTTCTTCTTCTTGGCAGTTCTGAATGTTTCTTCTCTCCATGATGGCTTATGATCGCTTGT
 GGCCATCTGTAACCTCTCCATTATTCAGTCATAATGAACAGGTCCCTATGCTTGTGGATG
 GCCATAGGCTCTTGGATGTCCGGTGTCTCTGTGTCTATGCTACAGACAGCTTGGATGATGG
 25 CCCTTCTTTCTGTGGACAAATGCCGTGGACCACTTTTCTGTGATGGTCCCCAGTGTTA
 AAACAGTCACAGTGGATAACAACCATGTATGAAATGCAAGCACTTGCCTCCACACTCCTGT
 TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCGCATTATCATAACAATTCTG
 AGGATGTCCTCTGCCACTGGCCGCCAGAAGGCATTTTCTACTTGTCTCCTCACACCTCATGT
 GGTGTCCCTCTTCTACGGAACAGCCAGTCTGACCTACCTGCGGCCAAATCAAACCACTCC
 30 CCTGAGAGCAAGAAGCTAGTGTCTTGTCTTACACTGTCATCACACCTATGCTAAACCCCA
 TCATCTACGGCCTGAGGAACAATGAAGTGAAAGGGGCTGTCAAGAGGACAATCACTCAA
 AAGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)

AOLFR97 sequences:

35 MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSFMVVPSFSIAEHWRRMKGANLSQGMFEL
 LGLTTDPQLQRLFLVFLGMYTATLLGNLVMFLLHVSATLHTPMYSLKLSFLDFCYSSTVV
 PQLVNFLAKRKVISYFGCMTQMFFYAGFATSECYLIAAMAYDRYAAICNPPLYSTIMSPEVC
 ASLIVGSYSAGFLNSLIHTGCFSLKFCGAHVVTHFFCDGPPILSLSCVDTSLCEILLFIFAGFNLLS
 CTLTILISYFLILNTILKMSSAQGRFKAFSTCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRIVA
 40 VIYTVVIPVLNPLMYSRLNKDVKKALIKVWGRKTME (SEQ ID NO: 181)

ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT
 CCTTAGGCAGAAATTAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC
 TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT
 45 GGAGTTTGAGCTCTTGGGCCTCACCCTGACCCCCAGCTCCAGAGGCTGCTTCTCGTGGTG
 TTCCTGGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTCATGTTCTCTCTGATCCATG
 TGAGTGCCACCCTGCACACCCCATGTACTCCCTCCTGAAGAGCCTCTCTTCTTGGATTC
 TGCTACTCTCCACGGTGTGCCCCAGACCCTGGTGAACCTTCTTGGCCAAGAGGAAAGTGA
 TCTCTTATTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTTGCCACCACTGATGC
 50 TATCTCATCGCTGCCATGGCCTATGACCGCTATGCGCTATTTGTAACCCCTGCTCTACTC
 AACCATCATGTCTCCTGAGGTCTGTGCTCGCTGATTGTGGGCTCCTACAGTGCAGGATTC
 CACTCACTTCTTCTGTGATGGGCCACCCATCCTGCTTGTCTGTGTAGACACCTCACTGT
 GTGAGATCCTGCTCTTCAATTTTGTGTTTCAACCTTTTGTGCTGCACCTCACCCTCTTG
 55 ATCTCCTACTTCTTAATTTCTCAACCCATCCTGAAATGAGCTCGGCCAGGGCAGGTTTA
 AGGCATTTTCCACCTGTGCATCCACCTCACTGCCATCTGCTCTTCTTGGCACAACACTT

TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCAGGACCGCACAGTTGCTGTCA
TCTACACAGTGGTGATCCAGTGCTGAACCCCTCATGTACTCTTTGAGAAACAAGGATGT
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

5 **AOLFR98 sequences:**

MRGFNKTTVVVTQFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLEI
LSFSESCYTFVIIPQLLVHLLSDTKTISFMACATQLFFFLGFACTNCLLIAMGYDRYVAICHPLR
YTLIINKRLGLELISLSGATGFFIALVATNLICDMRFCGPNRVNHYFCDMAPVIKLACTDTHVKE
LALFSLVIMVPFLLILISYGFIVNTILKIPSAEGKKAFTVCASHLTVFVHYGCASIIYLRPKSK
10 SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)

ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGTTTCTCCAGCC
TGGGGGAGCTCCAGCTGCTGCTTTTGTGATCTTTCTTCTCCTATACTTGACAATCCTGGTG
GCCAATGTGACCATCATGGCCGTTATTCGCTTCAGCTGGACTCTCCACACTCCCATGTATG
15 GCTTTCTATTTCATCCTTTTCATTTTCTGAGTCCTGCTACACTTTTGTGATCATCCCTCAGCTGC
TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT
CTTTTCTTGGCTTTGCTTGCACCAACTGCCTCCTCATTGCTGTGATGGGATATGATCGCT
ATGTAGCAATTTGTGACCCCTCTGAGGTACACACTCATCATAAACAAGGCTGGGGTTGGA
GTTGATTTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATT
20 GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAACCCTATTTCTGTGACATGGCACCTGT
TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTTATTAGCCTCAGCATC
CTGGTAATTATGGTGCCTTTTCTGTAAATTCTCATATCCTATGGCTTCATAGTTAACACCAT
CCTGAAGATCCCCTCAGCTGAGGGCAAGAAGGCCTTTGTCACTGTGCCTCACATCTCACT
GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC
25 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTACTCCCTTACTTAATCCT
CTTGTCTACAGTCTGAGGAACAAAGAGGTAAAACTGCATTGAAAAGAGTTCTTGGAATG
CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

AOLFR99 sequences:

30 MERVNETVVREVI FLGFSSLARLQQLFVIFLLLYLFTLGTNAIISTIVLDRALHIPMYFFLAILSC
SEICYTFIIVPKMLVDLLSQKKTISFLGCAIQMFSFLFLGCSHSFLLAVMGYDRYIAICNPLRYSV
LMGHGVCMGLVAAACACGFTVAQIITSLVFHLPFYSSNQLHHFFCDIAPVLKLASHHNHFSQIV
IFMLCTLVLAIPLLLILVSYVHILSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFIYLRPQSNY
SSSQDALISVSYTIITPLFNPMIYSLRNKEFKSALCKIVRRTISLL (SEQ ID NO: 185)

35 ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTCATCTTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCCTGCTCCTCTACCTGTTCACTCTGGGCACC
AATGCAATCATCATTTCCACCATTGCTCTGGACAGGGCCCTTCATATCCCCATGTACTTCTT
CCTTGCCATCCTCTCTTGCTCTGAGATTTGCTACACCTTCATCATTGTACCCAAGATGCTGG
40 TTGACCTGCTGTCCCAGAAGAAGACCATTCTTTCTGCTGGGCTGTGCCATCCAAATGTTTTCC
TTCCTCTTCCTTGCTGCTCTCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT
AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA
GTGGCTGCTGCCTGTGCCTGTGGCTTCACTGTTGCACAGATCATCACATCCTTGGTATTTCA
CCTGCCTTTTTATTCTCCAATCAACTACATCACTTCTTCTGTGACATTGCTCCTGCTCTCA
45 AGCTGGCATCTCACCATAACCACTTTAGTCAGATTGTCATCTTCATGCTCTGTACATTGGTC
CTGGCTATCCCCTTATTGTTGATCTTGGTGTCTATGTTACATCCTCTCTGCCATACTTCA
GTTTCCTTCCACACTGGGTAGGTGCAAAGCTTTTCTACCTGTGTATCTCACCTCATTATTG
TCACTGTCCACTATGGCTGTGCCTCCTTTATCTACTTAAGGCCTCAGTCCAATACTCTCTCA
AGCCAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATGA
50 TTTATAGCTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAAAATTGTGAGAAGAACAAT
TTCCTGTTGTAA (SEQ ID NO: 186)

AOLFR101 sequences:

MDTGNWSQVAEFILGFPHLQGVQIYFLLLLLLIYLMTVLGNLLIFLVCLDSRLHTPMYHFVSI
55 LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL
HYPTLMTPTLCAEIAIGCWLGGLAGPVVEISLISRLPFCGPNRIQHVFCDFFPVLACTDTSINV

ATGGACACAGGGAAGTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCATCTCC
5 AGGGTGTCCAGATTATCTCTTCTCTTGTGTGCTTCTCATTTACCTCATGACTGTGTTGGGA
AACCTGTGATATTCTCTGGTGGTCTGCCTGGACTCCCGGCTTACACACCCATGTACCACT
TTGTACGATTCTCTCTTCTCAGAGCTTGGCTATACAGCTGCCACCATCCCTAAGATGCTG
GCAAACCTTGCTCAGTGAGAAAAAGACCATTTCAATTCTCTGGGTGTCTCCTGCAGATCTATT
TCTTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCTACGATAGGTA
10 TTTAGCCATCTGCCGGCCCCCTCCACTACCCAACCCTCATGACCCCAACACTTTGTGTCAGAG
ATTGCCATTGGCTGTTGGTTGGGAGGCTTGGCTGGGCCAGTAGTTGAAATTTCTTGATT
CACGCCTCCCAATTCTGTGGCCCCAATCGCATTACGACGCTTTTGTGACTTCCCTCCTGTG
CTGAGTTTGGCTTGCAGTACGCTCTATAAATGTCCTAGTAGATTTGTATAAATTCCTG
CAAGATCCTAGCCACCTTCTGCTGATCCTCTGCTCCTATGTGCAGATCATCTGCACAGTGC
15 TCAGAATTCCTCAGCTGCCGGCAAGAGGAAGGCCATCTCCAGTGTGCTGCCCTCCACTTCAC
TGTGGTTCTCATCTTCTATGGGAGCATCCTTTCCATGTATGTGCAGCTGAAGAAGAGCTAC
TCACTGGACTATGACAGGCCCTGGCAGTGGTCTACTCAGTGCTCACACCCTTCTCAACC
CCTTCATCTACAGCTTGCGCAACAAGGAGATCAAGGAGGCTGTGAGGAGGCAGCTAAAGA
GAATTGGGATATTGGCATGA (SEQ ID NO: 188)

20 AOLFR102 sequences:
MPVGGKLVFNQSEPTFVFRAFTTATEFQVLLFLLFLLLYLMILCGNTAIIWVVCTHSTLRTPMYF
FLSNLSFLELCYTTVVVPLMLSNILGAQKPISLAGCGAQMFFVTLGSTDCFLLAIMAYDRYVAI
CHPLHYTLIMTRELCTQMLGGALGLALFPSLQLTALIFTLPFCGHHQEINHFLCDVPPVRLACA
25 DIRVHQAVLYVVSILVLTIPFLICVSYVFITCAILSIRSAEGRRRAFSTCSFHLTVVLLQYGCCSL
VYLRPRSSTSEDEDSQIALVYTFVTPLLNPLLYSLRNKDVKGALRSAIRKAASDAN (SEQ ID
NO: 189)

[illegible]

45 AOLFR103 sequences:
MAEMNLTIVTEFLLIAFTEYPEWALPLFLLLFMYLITVLGNLEMIILMDHQLHAPMYFLLSH
LAFMDVCYSSITVPQMLAVLLEHGAALSYTRCAAQFFLFTFFGSIDCYLLALMAYDRYLAVCQ
50 PLYVTILTQQARLSLVAGAYVAGLISALVRTVSAFTLSFCGTSEIDFIFCDLPPLLKLTGGEYSY
QEVLIIMFAIFVIPASMVVILVSYLFIIVAIMGIPAGSQAKTFSTCTSHLTAVSLFFGTLIFMYLRG
NSDQSSEKNRVVSVLYTEVIPMLNPLIYSLRNKEVKEALRKILNRAKLS (SEQ ID NO: 191)
GTTTATTCGATTCACTGAATATC

ATGGCAGAGATGAACCTCACCTTGGTGACCGAGTTCCTCCTTATTGCATTCACTGAATATC
CTGAATGGGCACTCCCTCTCTTCTTGTATTATTTATGTATCTCATCACCGTATTGGGG
AACTTAGAGATGATTATTCTGATCCTCATGGATCACCAGCTCCACGCTCCAATGTATTTCTT
TCTGAGTCACCTCGCTTTCATGGACGTCTGCTACTCATCTATCACTGTCCCCAGATGCTGG

CAGTGTCTGCTGGAGCATGGGGCAGCTTTATCTTACACACGCTGTGCTGCTCAGTTCTTTCT
 GTTCACCTTCTTTGGTTCCATCGACTGCTACCTCTTGGCCCTCATGGCCTATGACCGCTACT
 TGGCTGTGTGCCAGCCCCTGCTTTATGTACCATCCTGACACAGCAGGCCCGCTTGAGTCT
 TGTGGCTGGGGCTTACGTTGCTGGTCTCATCAGTGCCTTGGTGCGGACAGTCTCAGCCTTC
 5 ACTCTCTCCTTCTGTGGAACCAAGTGAGATTGACTTTATTTTCTGTGACCTCCCTCCTCTGTT
 AAAGTTGACCTGTGGGGAGAGCTA CACTCAAGAAGTGCTGATTATTATGTTTGCCATTTTT
 GTCATCCCTGCTTCCATGGTGGTGATCTTGGTGTCTTACCTGTTTATCATCGTGGCCATCAT
 GGGGATCCCTGCTGGAAGCCAGGCCAAGACCTTCTCCACCTGCACCTCCCACCTCACTGCT
 GTGTCACTCTTCTTTGGTACCCTCATCTTCATGTACTTGAGAGGTAACCTCAGATCAGTCTTC
 10 GGAGAAGAATCGGGTAGTGTCTGTGCTTTACACAGAGTGCATCCCATGTTGAATCCCCTC
 ATCTACAGCCTGAGGAACAAGGAAGTGAAGGAGGCCCTGAGAAAAATTCTCAATAGAGCC
 AAGTTGTCCTAA (SEQ ID NO: 192)

AOLFR105 sequences:

15 MQGLNHTSVSEFILVGFSAPPHLQLMLFLLFLLMYLFTLLGNLLIMATVWWSERSLHMPMYLFLC
ALSITEILYTVAIIPRMLADLLSTQRSIAFLACASQMFFSFSFGFTHSFLLTVMGYDRYVAICHPL
RYNVLMSLRGCTCRVGCSWAGGLVMGMVVTSAIFHLAFCGHEIHHFFCHVPPLLKLACGDD
VLVVAKGVLVCITALLGCFLILLISYAFIVAAILKIPSAEGRNKAFTSCASHLTVVVVHYGFAS
20 VIYLPKPGQSPGDTLMGITYTVLTPFLSPIIFSLRNKELKVAMKKTCFTKLFPQNC (SEQ ID
NO: 193)

ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCACTCTCGTTGGCTTCTCTGCCCTCCC
CCACCTCCAGCTGATGCTCTTCCCTGCTGTTCCCTGCTGATGTACCTGTTACGCTGCTGGGCA
ACCTGCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATGTACCTCTT
25 CCTGTGTGCCCTCTCCATCACCGAGATCCTCTACACCGTGGCCATCATCCCGCGCATGCTG
GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCTCGCCCTGTGCCAGTCAGATGTTCTT
CTCCTTCAGCTTCGGCTTACCCACTCCTTCCCTGCTCACTGTCATGGGCTACGACCGCTACG
TGGCCATCTGCCACCCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG
GGTGGGCTGCTCCTGGGCTGGTGGCTTGGTCATGGGGATGGTGGTGACCTCGGCCATTTC
30 CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTTCTTCTGCCACGTGCCACCTCTGTT
GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGTAT
CACGGCCCTGCTGGGCTGTTTTCTCCTCATCTCCTCTCCTATGCCTTCATCGTGGCCGCCA
TCTTGAAGATCCCTTCTGCTGAAGGTCGGAACAAGGCCTTCTCCACCTGTGCCTCTCACCT
CACTGTGGTGGTCGTGCACTATGGCTTTGCCTCCGTCAATTTACCTGAAGCCCAAAGGTCCC
35 CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGTCCTCACACCCTTCTCA
GCCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTCGCCATGAAGAAGACTTGCTT
CACCAAACCTCTTCCACAGAACTGCTGA (SEQ ID NO: 194)

AOLFR106 sequences:

40 METANYTKVTEFVLVTGLSQTPEVQLVLFVIFLSFYLFILPGNIICTISLDPHLTSPMYFLLANLA
FLDIWYSSITAPEMLIDFFVERKIIISFDGCIQLFFLHFAGASEMFLLTVMAFDLTYAICRPLHYA
TIMNQRLCCILVALSWRGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
ICSSGLISVVCLIALMSYAFLLALFKKLSGSGENTNRAMSTCYSHITIVVLMFGPSIYTYARPF
SFSLDKVVSVFNTLIFPLRNPIIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

45 ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
CAGAGGTCCAAGTCTCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
AATATCCTTATCATTTGCACCATCAGTCTAGACCCTCATCTGACCTCTCCTATGTATTTCTT
50 GTTGGCTAATCTGGCCTTCTTGATATTTGGTACTCTTCCATTACAGCCCCTGAAATGCTCA
TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGATGGATGCATTGCACAGCTCTTCTT
CTTACACTTTGTCTGGGGCTTCGGAGATGTTCTTGCTCACAGTGATGGCCTTTGACCTCTACA
CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGCTCTCTGCTGTATCCTG
GTGGCTCTCTCCTGGAGGGGGGCTTCATTCTATCATACAGGTGGCTCTCATTTGTTT
GACTTCCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACAGAGTTGT
55 CCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGCGTCTG
ATCTCTGTGGTGTGTTTGATTGCTCTGTTAATGTCCTATGCCTTCTTCTGGCCTTGTTCAA

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5 GAAACTTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACATT
 ACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCGTT
 TTCCCTAGATAAAGTGGTGTCTGTGTTCAATACTTTAATATCCCTTTACGTAATCCCATT
 TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGGTCACCAATATA
 TTTTGTGTAAAGAGAAGTGA (SEQ ID NO: 196)

AOLFR107 sequences:

10 MELWNFTLGSGFILVGILNDSGSPELLCATITILYLLALISNGLLLLAITMEARLHMPMYLLLGO
 LSLMDLLFTSVVTPKALADFLRRENTISFGGALQMFLALTMGGAEDLLAFMAYDRYVAICH
 PLTYMTLMSSRACWLMVATSWILASLSALIYTVYTMHYPCRAQEIRHLLCEIPHLKLVACAD
 TSRYELMVYVMGVTFILPSLAAILASYTQILLTVLHMPSNEGRKKALVTCSSHLTUVGMFYGA
 ATFMVYLPSSFHSTRQDNISVFYITVTPALNPLIYSLRNKEVMRALRRVLGKMYLPAHSTL
 (SEQ ID NO: 197)

15 ATGGAGCTCTGGAACCTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA
 GTGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACTTGTGGCCCTGATCAG
 CAATGGCCTACTGCTCCTGGCTATCACCATGGAAGCCCGCTCCACATGCCCATGTACCTC
 CTGCTTGGGCAGCTCTCTCATGGACCTCCTGTTACATCTGTTGCTACTCCCAAGGCCCT
 TGCGGACTTTCTGCGCAGAGAAAACACCATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTT
 20 CTGGCACTGACAATGGGTGGTGGTGGAGACCTCCTACTGGCCTTCATGGCCTATGACAGGT
 ATGTGGCCATTTGTATCCTCTGACATACATGACCCCTCATGAGCTCAAGAGCCTGCTGGCT
 CATGGTGGCCACGTCTGATCCTGGCATCCCTAAGTGCCCTAATATATACCGTGTATACC
 ATGCACTATCCCTTCTGACGGGCCAGGAGATCAGGCATCTTCTGTGAGATCCCACACT
 TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT
 25 GACCTTCTGATTCCTCTCTTGTGCTATACTGGCCTCCTATACACAAATTCTACTACTG
 TGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTGTACCTGCTCTTCCACCT
 GACTGTGGTTGGGATGTTCTATGGAGCTGCCACATTCATGTATGTCTTGCCAGTTCCCTCC
 ACAGCACCAGACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAA
 TCCACTCATCTACAGCCTGAGGAATAAGGAGGTCTGCGGGCCTTGAGGAGGGTCTGGG
 30 AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)

AOLFR108 sequences:

35 MCSFFLCQTKQAKISMGEENQTFVSKFIFLGLSQDLQTLQILLFILHLYLLTVLGNQLIIMFLD
 SRLHTPMYFFLRNLSFADLCFSTSIQVVLVHFLVKRKTISFYGCMTQIIVFLLVGTECALLAV
 MSYDRYVAVCKPLYYSTIMTQRVCLWLSFRSWASGALVSLVDTSTFHLPHYWGQNIINHYFCE
 PPALLKLASIDTYSTEMAIFSMGVVILLAPVSLILGSYWNIISTVIQMQSGEGRKAFSTCGSHLI
 VVVLFGSGIFTYMRPNSKTTKELDKMISVFYTAFTPMLNPIIYSLRNKDVKGALRKLVGGRKC
 FSHRQ (SEQ ID NO: 199)

40 ATGTGTTCTTTTTCTTGTGCCAAACAGGTAAACAGGCCAAAAATATCAATGGGAGAAGAAA
 ACCAAACCTTTGTGTCCAAGTTTATCTTCTGGGTCTTTCACAGGACTTGCAGACCCAGAT
 CCTGCTATTTATCCTTTTCTCATCTTATCTGCTGACCGTGCTTGGAAACCAGCTCATCA
 TCATTCTCATCTTCTGGATTCTCGCCTTCACTCCCATGTATTTTTCTTAGAAATCTCT
 CCTTGCAGATCTCTGTTTCTCTACTAGCATTGTCCCTCAAGTGTTGGTTCACTTCTTGGTA
 45 AAGAGGAAAACCATTTCTTTTTATGGGTGTATGACACAGATAATTGTCTTCTTCTGTTG
 GGTGTACAGAGTGTGCGCTGCTGGCAGTGATGTCCTATGACCGGTATGTGGCTGTCTGCAA
 GCCCCTGTACTACTCTACCATCATGACACAACGGGTGTGTCTCTGGCTGTCTCAGGTCTT
 GGGCCAGTGGGGCACTAGTGTCTTTAGTAGATAACAGCTTTACTTTCCATCTTCCCTACTG
 GGGACAGAATATAATCAATCACTACTTTTGTGAACCTCCTGCCCTCCTGAAGCTGGCTTCC
 50 ATAGACACTTACAGCACAGAAATGGCCATCTTTCAATGGGCGTGGTAATCCTCCTGGCCC
 CTGTCTCCCTGATTCTTGGTTCTTATTGGAATATTATCTCCACTGTTATCCAGATGCAGTCT
 GGGGAAGGGAGACTCAAGGCTTTTTCCACCTGTGGCTCCCATCTTATTGTTGTTGTCTCTT
 CTATGGGTCAGGAATATTCACCTACATGCGACCAAACTCCAAGACTACAAAAGAACTGGA
 TAAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCATAATTTATAGC
 55 TTGAGGAACAAAGATGTCAAAGGGCTCTCAGGAACTAGTTGGGAGAAAGTGCTTCTCT
 CATAGGCAGTGA (SEQ ID NO: 200)

AOLFR109 sequences:

- MLRNGSIVTEFILVGFQSSSTRALLFALFLALYSLTMAMNGLIIFITSWTDPKLNSPMYFFLG
 5 HSLSLDVCFITTTIPQMLIHLVVRDHIVSFVCCMTQMYFVFCVGVAECILLAFMAYDRYVAICY
 PLNYVPIISQKVCVRLVGTAFFGLINGIFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL
 WAIFADAIVVILSPMVLTVTSYVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN
 PHSTHGPDKDKPFSLLYTIITPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPSV (SEQ ID NO:
 201)
- 10 ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTCAGCAGAGCTCCA
 CTTCCACACGAGCATTGCTCTTTGCCCTCTTCTTGGCCCTCTACAGCCTCACCATGGCCATG
 AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT
 TCTTCTCGGCCATCTGTCTCTCCTGGATGTCTGCTTCATCACCCTACCATCCCACAGATG
 TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT
 15 ACTTTGTCTTCTGTGTTGGTGTGGCCGAGTGCATCCTCTTGGCTTTCATGGCCTATGACCGT
 TATGTTGCTATCTGCTACCCACTTAAGTATGTCCCGATCATAAGCCAGAAGGTCTGTGTCA
 GGCTTGTGGGAAGTGCCTGGTCTTTGGGCTGATCAATGGCATCTTTCTCGAGTATATTTT
 ATTCCGAGAGCCCTTCCGAGAGACAACCACATAGAAAGCTTCTTCTGTGAGGCCCCCAT
 GTGATTGGCCTCTCTGTGGGGACCCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA
 20 TCGTGGTAATTCTCAGCCCCATGGTGCTCACTGTCACCTTCTATGTGCACATCCTGGCCACC
 ATCCTCAGCAAAGCCTCCTCCTCAGGTGCGGGGAAGACTTTCTCTACTTGTGCCTCTCACC
 TGACTGTGGTCATCTTTCTCTACACTTCAGCTATGTTCTCTTACATGAACCCCCACAGCACA
 CATGGGCCTGACAAAGACAAACCTTTCTCCCTCCTGTACACCATCATTACCCCATGTGCA
 ACCCATCATTTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG
 25 GAAGAACCAGGCTGGCCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

AOLFR110 sequences:

- MKIANNTVVTEFILLGLTQSQDIQLLVFVLILIFYLIILPGNFLIIFTIRSDPGLTAPLYLFLGNLAFL
 30 DASYSFIVAPRMLVDFLSEKKVISYRGCTQLFFLHFLGGEGLLLVMFAFDRIAICRPLHCST
 VMNPRACYAMMLALWLGGFVHSIIQVVLRLPFCGPNQLDNFFCDVRQVIKLA CTDMFVVEL
 LMVFNSGLMTLLCFLGLLASYAVILCHVRRASEGKNKAMSTCTTRVIIIILMFGPAIFIYMCPP
 RALPADKMVSLFHTVIFPLMNPMIYTLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO:
 203)
- 35 ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC
 AAGATATTCAGCTCTTGGTCTTTGTGCTGATCTTAATTTTCTACCTTATCATCCTCCCTGGA
 AATTTTCTCATTATTTTACCATAAAGGTCAGACCCTGGGCTCACAGCCCCCTCTATTTATT
 TCTGGGCAACTTGGCCTTCTGAGTGCATCCTACTCCTTCAATTGTGGCTCCCAGGATGTTGG
 TGGACTTCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT
 40 CTTGCACTTCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTAC
 ATCGCCATCTGCCGGCCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA
 TGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCCTCATCCTC
 CGCTTGCTTTTTGTGGCCCAAACCAGCTGGACAACTTCTTCTGTGATGTCCGACAGGTCA
 TCAAGCTGGCTTGACCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT
 45 GATGACACTCCTGTGCTTTCTGGGGCTTCTGGCTTCTATGCAGTCATCCTCTGCCATGTTT
 GTAGGGCAGCTTCTGAAGGGAAGAAACAAGGCCATGTCCACGTGCACCACTCGTGTCATTA
 TTATACTTCTTATGTTTGGACCTGCTATCTTCATCTACATGTGCCCTTTTACGGGCCTTACCA
 GCTGACAAGATGGTTTCTCTCTTTTACACAGTGATCTTTCCATTGATGAATCCTATGATTTA
 TACCCTTCGCAACCAGGAAGTGAAAACCTCCATGAAGAGGTTATTGAGTCGACATGTAGTC
 50 TGTCAAGTGGATTTTATAATAAGAACTGA (SEQ ID NO: 204)

AOLFR111 sequences:

- MCYIYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGFSTNKNMCIILHSILFLLIYLCALM
 55 GNVLIIMITTLDHHLHTPVYFLKNLSFLDLCLISVTA PKSIANSIHNNSISFLGCVSQVFLLSS
 ASAELLLLTVMSFDRYTAICHPLHYDVIMDRSTCVQRATVSWLYGGGLIAVMHTAGTFSLSYCG
 SNMVHQFFCDIPQLLAISCSENLIREIALILNVVLDFFCFIVIIITYVHVSTVKKIPSTEGQSKAY

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SICLPHLLVVFLSTGFIAYLKPASESPSILDAVISVFYTMPLPTFNPIIYSLRNKAIVKVALGMLIKG
 KLTCK (SEQ ID NO: 205)

5 ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT
 TTCTCTGCAGATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA
 TGGGGTTTTCTACCAATAAAAAATATGTGCATTTTGCATTGCTCTTCTTGTGATTAT
 TTGTGTGCCCTGATGGGGAATGTCTCATTATCATGATCACAACCTTGGACCATCATCTCC
 ACACCCCGTGTATTTCTTCTTGAAGAATCTATCTTCTTGGATCTCTGCCTTATTTTCTGCTG
 10 ACGGCTCCCAAATCTATCGCCAATCTTTGATACACAACAACCTCCATTTTCTTGGCTG
 TGTTTCCCAGGTCTTTTGTGCTTTCTCAGCATCTGCAGAGCTGCTCCTCCTCACGGTGA
 TGTCTTTGACCGCTATACTGCTATATGTCAACCTCTGCACTATGATGTATCATGGACAGG
 AGCACCTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGTCTGATTGCTGTGATGC
 ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAACATGGTCCATCAGTTCTTCTGT
 GACATCCCCAGTTATTAGCTATTTCTGCTCAGAAAATTTAATAAGAAATTGCACTCA
 15 TCCTTATTAATGTAGTTTGGATTCTGCTGTTTTATTGTATCATCATTTACCTATGTCCAC
 GTCTTCTACAGTCAAGAAGATCCCTCCACAGAAGGCCAGTCAAAAGCCTACTCTATT
 GCCTCCACACTTGTGTTGTGTTATTTCTTCCACTGGATTGCTTATCTGAAGCCA
 GCTTCAGAGTCTCCTTCTATTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCCC
 AACCTTAAATCCCATTATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG
 20 TTGATAAAGGGAAAGCTACCAAAAAGTAA (SEQ ID NO: 206)

AOLFR113 sequences:

MKFWHGFSSHLNPMFSSFLLYSLPWINTTIQAWNLCSLALPVWAMSGAGFLSCCYWHTCSP
 25 SVVTCSSSQSSDWMQLCTHLCTTSLVFFPSWSCGIQLPLSLRCLIFSRRKPFLLQDASFRPTSS
 TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTLCAMAAACWTCGFLCPISEVILASQLPF
 CAYNEIQHIFCDFPILLSACKDTSANILVDFAINAFILITFFIMISYARIIGA VLKIKTASGRKK
 AFSTCASHLAVVLIFFGSIIFMYVRLKKSYSLLDRTLAIVSVLTPMVNPIIYSLRNKEIKAIKR
 TIFQKGDKASLAHL (SEQ ID NO: 207)

30 ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTGTGCATTAACAGGA
 AAAAAGTCTCATTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
 CTCTCTCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTGGCTGGCTATCTCACTGA
 GTGCCATGTACATCATAGCCCTGTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
 35 TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTTCTGGCTGCTGTGGACATTGTA
 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
 CTTTAGTGCTTGTTCCTCAGATGTTTTGTGCTTACTAGCCATCTGCAAGCCTCTACACTACAAGA
 CTGCTGCTGACCATGGCTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
 GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
 40 AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGTT
 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCTTATTGCT
 GCAGTCTCTACAGTCTGATTGGTCTCTTATGGTGGGCTCTGATGTGGCCTTATTGCT
 GCCTCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
 AGCATTAAAGCATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
 45 GCATCCATCTATGCGGCTGGTGGGGCAGGATGTAGTGGCCTTGACACCCCAAGTCTGCTG
 TAGCTGACCTGTACGTGATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
 CAAACAACCTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCTCTTGGACATTCCAAC
 CTGGGTTCTATGA (SEQ ID NO: 208)

AOLFR114 sequences:

50 MERINHTSSVSEFILLGLSSRPEDQKTLFVFLIVYLVTITGNLLILAIRFNPHLQTPMYFFLSFLS
 LTDICFTTSVVPKMLMNFLSEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDYVAVCDPF
 HYVTTMSHHHCVLLVAFSCSFPHLSLLHTLLNRLTFCDNSVIHFLCDLSPVLKSCSSIFVN
 EIVQMTEAPIVLVTRFLCIAFSYIRILTTVLKIPSTSGKRKAFSTCGFYLTVVTLFYGSIFCVYLQ
 PSTYAVKDHVATIVYTVLSSMLNPFYSLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

55

ATGGAAAGAATCAACCACACCAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC
 GGCCTGAGGACCAAAAGACACTCTTTGTTCTCTTCCTCATCGTGTACCTGGTCACCATAAC
 AGGGAACCTGCTCATCATCTGGCCATTTCGCTTCAACCCCCATCTTCAGACCCCTATGTATT
 TCTTCTTGAGTTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCCAAGATG
 5 CTGATGAACTTCCTGTCAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGT
 ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTCATGGCCTTTGACCG
 CTATGTGGCCGTCTGTGACCCTTTCCACTATGTCAACCACCATGAGCCACCACCACTGTGTCC
 TGCTGGTGGCCTTCTCCTGCTCATTTCTCACCTCCACTCACTCCTGCACACACTTCTGCTG
 AATCGTCTCACCTTCTGTGACTCCAATGTTATCCACCACCTTTCTCTGTGACCTCAGCCCTGT
 10 GCTGAAATTGTCCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT
 ATTGTTTTGGTGACTCGTTTTCTCTGCATTGCTTTCTCTTATATACGAATCCTCACTACAGT
 TCTCAAGATTCCCTCTACTTCTGGGAAACGCAAAGCCTTCTCCACCTGTGGTTTTTACCTCA
 CCGTGGTGACGCTCTTTATGGAAGCATCTTCTGTGTCTATTTACAGCCCCCATCCACCTAC
 GCTGTCAAGGACCACGTGGCAACAATTGTTTACACAGTTTTGTTCATCCATGCTCAATCCTT
 15 TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA
 GATCCTAG (SEQ ID NO: 210)

AOLFR115 sequences:

MEGFYLRRSHELQGMGKPGRVNQTTVSDFLLLGLSEWPPEQPLLFGIFLGMVLTVMVGNLLII
 20 LAISSDPLHPTMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGLD
 NCLLAVMAYDRYVAICQLHYSTSMSPQLCALMLGVCWVLTNCPALMHTLLLTRVAFCAQK
 AIPHFYCDPSALLKLACSDTHVNELMIITMGLLFTVPLLLIVFSYVRIFWAVFVISSPGGRWKA
 FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLNRNDRMKEALG
 KLFVSGKTFFL (SEQ ID NO: 211)

ATGGAAGGTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA
 GTGAACCAAACCACTGTTTCAGACTTCCTCCTTCTAGGACTCTCTGAGTGGCCAGAGGAGC
 AGCCTCTTCTGTTTGGCATCTTCCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC
 ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTTCTTTCTGGCCAA
 30 CCTGTCAATTAAGTATGCTGCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAAACATTC
 ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGTCTTGACACAGCTATATTTCTCCTTATG
 TTTGGTGGCCTTGACAACTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT
 GCCAACCCTCCATTACAGCACATCTATGAGTCCCCAGCTCTGTGACTAATGCTGGGTGT
 GTGCTGGGTGCTAACCAACTGCTCCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT
 35 TTCTGTGCCAGAAAGCCATCCCTCATTTCTATTGTGATCCTAGTGCTCTCCTGAAGCTTGC
 CTGCTCAGATACCCATGTAAACGAGCTGATGATCATCACCATGGGCTGTGTTCTCCTACT
 GTTCCCCTCCTGCTGATCGTCTTCTCCTATGTCCGCATTTCTGGGCTGTGTTTGTCTCTC
 ATCTCCTGGAGGGAGATGGAAGGCCTTCTCTACCTGTGGTTCTCATCTCACGGTGGTTCTG
 CTCTTCTATGGGTCTCTTATGGGTGTGATTTACTTCTCCATCAACTTACTCTACAGAGAG
 40 GGAAAGTAGGGCTGCTGTTCTCTATATGGTGATTATTTCCACGCTAAACCCATTCAATTAT
 AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAAACTTTTTGTCAAGTGGAAAAACA
 TTCTTTTTATGA (SEQ ID NO: 212)

AOLFR116 sequences:

MDEANHSVVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFLLAN
 45 LSIINLVFCSSTAPKMIYDLFRKHKTISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH
 YLTIMNPQRCLFLVISWIIHHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV
 TANSGFISLASFLILISYIFLVTQKSSGGIFKAFLSAHVIVVVLVFGPLIFFYIFPPTSHLD
 KFLAIFDAVITPVLNPVIYTFRNKEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCTCCTGGGACTCTCTGACTCGC
 GGAAGATCCAGCTCCTCCTCTTCTCTTTTTCTCAGTGTTCTATGTATCAAGCCTGATGGGA
 AATCTCCTCATTGTGCTAACTGTGACCTCTGACCCTCGTTTACAGTCCCCCATGTACTTCTC
 GCTGGCCAACCTTTCCATCATCAATTTGGTATTTTGTTCCTCCACAGCTCCCAAGATGATTT
 55 ATGACCTTTTTCAGGAAGCACAAGACCATCTCTTTTGGGGGCTGTGTAGTTCAGATCTTCTT
 TATCCATGCAGTTGGGGGAACCTGAGATGGTGCTGCTCATAGCCATGGCTTTTGACCGATAT

GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT
TTTTAGTCATTTCTGGATTATAGGTATTATTCACTCAGTGATTGAGTTGGCTTTTGTGTA
GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTGTGATCTTCCTCGATTAT
5 CAAACTGGCTTGCATAGAGACCTACACATTGGGATTCATGGTTACTGCCAATAGTGGATT
ATTTCTCTGGCTTCTTTTAAATTCTCATAATCTCTTACATCTTTATTTGGTGACTGTTGAG
AAAAAATCTTCAGGTGGTATATTCAAGGCTTCTCTATGCTGTCAGCTCATGTCATTGTGG
TGGTTTTGGTCTTTGGGCCATTAATCTTTTCTATATTTTCCATTCCCACATCATCTTG
ATAAATTCCTTGGCATCTTTGATGCAGTTATCACTCCCGTTTTGAATCCAGTCATCTATACT
10 TTTAGAAATAAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC
AGTAAAATCTTTTAA (SEQ ID NO: 214)

AOLFR117 sequences:

MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLVISRLLAMTLGNSTEVTEFYLLGFGA
QHEFWCILFIVFLLIYVTSIMGNSGILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSFT
15 EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDVYVICKPLHYTVIMSRTVCIRLVAGSYI
MGSINASVQTGFTCSLSFCKSNSINHHFCDVPILALSCSNVDINIMLLVVFVGSNLIFTGLVVIFS
YIYIMATILKMSSSAGRKKSFTCASHLTAVTIFYGTLASYMYLQSHSNNSQENMKVAFIFYGTVI
PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215)

20 ATGAATAACACTATTGTATTTGTCATAAAAAATACAAATAGAAAAAAGTGACTTGAAATATA
GAGCCATTTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTCTGGGTCCTTCTCTTGGTC
ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCTATC
TTCTGGGATTTGGTGCCAGCATGAGTTTTGGTGTATCCTCTTCATTGTATCCTTCTCATC
TATGTGACCTCCATAATGGGTAATAGTGAATAATCTTACTCATCAACACAGATTCCAGAT
25 TTCAAACACTCACGTACTTTTTTCTACAACATTTGGCTTTTGTGATATCTGTTACACTTCT
GCTATCACTCCCAAGATGCTCCAAAGCTTCACAGAAGAAAAGAATTTGATATTATTTGAGG
GCTGTGTGATACAATTCTTAGTTTATGCAACATTTGCAACCAGTGACTGTTATCTCTGGCT
ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCTTCACTATACTGTAATCATGT
CCCGAACAGTCTGCATCCGTTTGGTAGCTGGTTCATACATCATGGGCTCAATAAATGCCTC
30 TGTACAAACAGGTTTACATGTTCACTGTCTTCTGCAAGTCCAATAGCATCAATCACTTTT
TCTGTGATGTTCCCCCTATTCTTGCTCTTTTCTGCAAGTCCAATAGCATCAATCACTTTT
CTTGTGTCTTTGTGGGATCTAACTTGATATTCAGTGGGTTGGTCGTCATCTTTCTCTCAT
CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAATCCTTCTCA
ACATGTGCTTCCACCTGACCGCAGTACCATTCTTCTATGGGACACTCTTACATGTATTT
35 GCAGTCTCATTCTAATAATCCCAGGAAAAATAGAAAGTGGCCTTTATATTTATGGCACA
GTTATTCCTATGTTAAATCCTTTAATCTATAGCTTGAGAAATAAGGAAGTAAAAGAAGCTT
TAAAAGTGATAGGAAAAAGTTATTTTAA (SEQ ID NO: 216)

AOLFR118 sequences:

40 MNHMSASLKISNSSKFQVSEFILLGFPPIHSWQHWLSLPLALLYLSALAANTLILIIHWQNP SLQQ
PMYIFLGILCMVDMGLATTIIPKILAFWFDKVISLPECFAQIYAIHFFVGMESGILLCMFDRY
VAICHPLRYPSTVSSLILKATLFMVLRLNGLFVTPVLAQRDYCSKNEIEHCLCSNLGVTS LA
CDDRRPNSICQLVLA WLGMSDLSLILSYLILYSVRLNSAEAAAKALSTCSSHLTLILFFYTIV
45 VVISVTHLTEMKATLIPVLLNLHNIIPPSLNPTVYALQTKELRAAFQKVLFAITKEIRS (SEQ ID
NO: 217)

ATGAATCATATGTCTGCATCTCTCAAAATCTCCAATAGCTCCAAATCCAGGTCTCTGAGTT
CATCCTGCTGGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCCTGGCA
CTACTGTATCTCTCAGCACTTGCTGCAAAACACCTCATCTCATCATCTGGCAGAACCC
50 TTCTTTACAGCAGCCCATGTATATTTTCTTGGCATCCTCTGTATGGTAGACATGGGTCTGG
CCACTACTATCATCCCTAAGATCCTGGCCATCTTCTGGTTTGTGCAAGGTTATTAGCCTC
CCTGAGTGCTTTGCTCAGATTTATGCCATTCACTTCTTGTGGGCATGGAGTCTGGTATCCT
ACTCTGCATGGCTTTTGTAGATATGTGGCTATTTGTCAACCTCTTCGCTATCCATCAATTG
TCACCAGTTCCTTAATCTTAAAAGCTACCCTGTTTGTGCTGAGAAATGGCTTATTTGTG
55 ACTCCAGTGCCTGTGCTTGAGCACAGCGTGATTATTGCTCCAAGAAATGAAATTGAACACT
GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT

TTGCCAGTTGGTTCTGGCATGGCTTGAATGGGGAGTGATCTAAGTCTTATTATACTGTCA
 TATATTTTGATTCTGTACTCTGTACTTAGACTGAACTCAGCTGAAGCTGCAGCCAAGGCC
 TGAGCACTTGAGTTCACATCTCACCCCTCATCTTTCTTTTACACTATTGTTGTAGTGATT
 TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTTCTACTTAATGTGTTGC
 5 ACAACATCATCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAAGAAGCTTAG
 GGCAGCCTTCCAAAAGGTGCTGTTTGCCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:
 218)

AOLFR119 sequences:

10 MPLFNSLCWFPTIHVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP
 MYFFFGHALSLIDLLTCTTTLPNALCIFWFSLEINFNACLAQMFFVHGFTGVESGVMLMALD
 RYIAICYPLRYATTLTNPIAKAELATFLRGVLLMIPFPFLVKRLPFCQSNISHTYCDHMSVVKL
 SCASIKVNVIYGLMVALLIGVFDICCSLSYTLILKAAISLSSSDARQKAFSTCTAHISAIHTYVPA
 FFTFFAHRFGGHTIPPSLHIIVANLYLLPPTLNPIVYGVKTKQIRKSVIKFFQGDKGAG (SEQ ID
 15 NO: 219)

ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT
 TCTTAATGGAATACCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCACTCTGCACA
 ATGTACATCATCTTCCTTGTTGGGGAATCTTGGTCTTGTTGACCTCATTATTATGAGGAGTC
 20 CTTACATCATCCGATGTATTTTTTTTTTGGCCATGCTCTCTCCCTCATTGACCTCCTTACCTG
 CACCACCACTCTACCCAATGCACTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTCA
 ATGCTTGCTTGGCCCAGATGTTCTTTGTTTCATGGGTTACAGGTGTGGAGTCTGGGGTGCT
 CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCCTTTGCGTTATGCTACCACAC
 TCACCAACCCTATCATTGCCAAGGCTGAGCTTGCCACCTTCTGAGGGGTGTATTGCTGAT
 25 GATTCCCTTCCCAATTCTTGGTTAAGCGTTTGCCTTTCTGCCAAAGCAATATTATCTCCCAT
 CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT
 CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTTGACATTTGTTGTATATCTTTGCTCTT
 ACACTTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT
 CAGCACCTGCACTGCCCATATATCTGCCATCATCATCACCTATGTTCCAGCATTCTTCACTT
 30 TCTTTGCCACCGTTTTTGGGGGACACACAATTCCCCCTTCTCTTACATCATTGTGGCTAAT
 CTTTATCTTCTTCTTCCCCCAACTCTAAACCCTATTGTTTATGGAGTAAAGACAAAACAGAT
 ACGCAAGAGTGTCTATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

AOLFR120 sequences:

35 MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAAILVVGLDHRLRRPMPYF
 FLTHLSCLEIWTYSVTVPKMLAGFIGVDGGKNISYAGCLSQLFIFTFLGATECFLLAAMAYDRY
 VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPILPYLLSQLTFCGPNVIDHFSCDASPLLALS
 CSDVTWKETVDFLVSLAVLLASSMVIASVYGNIVWTLHIRSAAERWKAFSTCAAHLTVVSLF
 YGTLFFMYVQTKVTSSINFNKVVSFYSVVTPLNPLIYSLRNKEVKGALGRVFSLNFWKGQ
 40 (SEQ ID NO: 221)

ATGCAACCATATACCAAAAACCTGGACCCAGGTAACCTGAATTTGTCATGATGGGCTTTGCTG
 GCATCCATGAAGCACACCTCCTCTTCTCATACTCTTCTCACCATGTACCTGTTACCTTG
 GTGGAGAATTTGGCCATCATTTTAGTGGTGGGTTTGGACCACCGACTACGGAGACCCATGT
 45 ATTTCTTCTGACACACTTGTCTGCCTTGAAATCTGGTACACTTCTGTTACAGTGCCCAAG
 ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAATATCTCTTATGCTGGTTGCCTAT
 CCCAGCTCTTCATCTTACCTTTCTTGGGGCAACTGAGTGTTCCTACTGGCTGCCATGGCC
 TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGTCCTGGGGCAC
 CTGCATCCGTCTGGCAGCTGCCTGTTGGCTGGTAGGTTTCTCACACCCATCTTGCCAATCT
 50 ACCTCTTGCTCAGCTAACATTTTGTGGCCCAAATGTCATTGACCATTCTCCTGTGATGCC
 TCACCTTGCTAGCCTTGTCGTGCTCAGATGTCACTTGGAAGGAGACTGTGGATTTCTGG
 TGTCTCTGGCTGTGCTACTGGCCTCCTCTATGGTCAATTGCTGTGTCCTATGGCAACATCGTC
 TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTTCTCTACCTGTGCAG
 CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTCTTTATGTATGTCCAGACCAAG
 55 GTGACCTCCTCCATCAACTTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTACGCCCAT

GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTGAGTC
TTTTCTCTCAACTTTTGAAGGGACAGTGA (SEQ ID NO: 222)

AOLFR121 sequences:

5 MKRKNFTEVSEFIFLGFSSFGKHQITLFFVFLTVYILTLVANIIVTICIDHHLHTPMYFFLSMLA
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFFVILATNNCFLLTAMGYDRYVAICRPLRY
TVIMSKGLCAQLVCGSFGIGLTMAVLHVTAMFNLPFCGTVVDHFFCDIYPVMKLSCIDTTINEII
NYGVSSFVIFVPIGLIFISYVLVISSILQIASAEGRKKTFATCVSHLTVVIVHCGCASIAYLKPKSES
SIEKDLVLSVTYTIITPLNPPVYSLRNKEVDALCRVVGRNIS (SEQ ID NO: 223)

10 ATGAAGAGAAAGAACTTCACAGAAGTGTGAGAATTCATTTTCTGGGATTTTCTAGCTTTG
GAAAGCATCAGATAACCCTCTTTGTGGTTTTCTTAAGTGTCTACATTTTAACTCTGGTTGCT
AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTTCTT
CCTAAGCATGCTGGCTAGTTCAGAGACGGTGTACACACTGGTCATTGTGCCACGAATGCTT
15 TTGAGCCTCATTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT
TTTTGTTATCTTGGCCACTAATAAATGCTTCTGCTTACTGCAATGGGGTATGACCGCTATG
TGGCCATCTGCAGACCCCTGAGATACACTGTCATCATGAGCAAGGGACTATGTGCCACGCT
GGTGTGTGGGTCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTTT
AATTTGCCGTTCTGTGGCACAGTGGTAGACCATTCTTTTGTGACATTTACCCAGTCATGA
20 AACTTTCTTGCATTGATAACCACTATCAATGAGATAATAAATTATGGTGTAAGTTCATTTGT
GATTTTTGTGCCCATAGGCCTGATATTTATCTCCTATGTCCTTGTGCTCTCTCCACCTCACTG
AAATTGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCACCTCACTGT
GGTTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAGTTCA
ATAGAAAAAGACCTTGTCTCTCAGTGACGTACACCATCATCACTCCCTGTGTAACCCCTG
25 TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA
ATATTTCTTAA (SEQ ID NO: 224)

AOLFR122 sequences:

30 MEWENQTILVEFFLKGHVSHPRELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTSIPSTLVSLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMAFDYVAICNPLR
YPIIMSKNA YVPMAGVSWFAGIVNSAVQTTFFVQLPFCRKNVINHFSCEILAVMKLACADISGN
EFLMLVATILFTLMPLLIVISYSLIISILKIHSEGRSKAFSTCSAHLTVIIFYGTILFMYMKPKS
KETLNSDDLDATDKIISMFGVMTMPMNPLIYSLRNKDVKEAVKHLNRRFFSK (SEQ ID NO:
225)

35 ATGGAATGGGAAAACCAACCAATTCTGGTGAATTTTTCTGAAGGGACATTCTGTTCAAC
CAAGGCTTGAGTACTCTTTTTGTGCTAATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCTCCACACTAG
40 TGAGCTTCCTTTCAGAAAGAAAGACCATTTCTTTTTCTGGCTGTGCAATGATGGCCTTGTGACCGCTATG
GGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTGTGACCGCTATG
TGGCTATCTGCAACCCCTCTGAGATATCCCATCATCATGAGCAAGAATGCCTATGTACCCAT
GGCTGTTGGGTCTGGTTTGCAGGATTGTCAACTCTGCAGTACAAACTACATTTGTAGTA
CAATTGCCTTTCTGCAGGAAGAATGTCATCAATCATTTCTCATGTGAAATTCTAGCTGTGAT
45 TTCACATTGATGCCACTGCTCTTGATAGTATCTTACTCATTAAATCATTTCCAGCATCCT
CAAGATTCACTCCTCTGAGGGGAGAAGCAAGCTTTCTCTACCTGCTCAGCCCATCTGACT
GTGGTCATAATATTCTATGGGACCATCCTCTCATGTATATGAAGCCCAAGTCTAAAGAGA
CACTTAATTGAGATGACTGGATGCTACCGACAAAATTATCCATGTTCTATGGGGTGAT
50 GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT
AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)

AOLFR123 sequences:

55 MYRFTDFDVSNISIYLNHVLFFYTTQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLCL
IMYMILLGNSLLIITILDSRLHTPMYFFLGNLSFLDICYTSSSIPPLIIFMSERKSISFIGCALQM
VVSGLGSTECVLLAVMAYDHYVAICNPLRYSIIMNGVLYVQMAAWSWIIGCLTSLLOQTVLT

MMLPFCGNNVIDHITCEILALLKLVCSDITINVLIMTVTNIVSLVILLLLIFISYVFILSSILRINCAE
GRKKAFTCSAHSIVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV
KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

- 5 ATGTACAGATTTACAGATTTTGATGTATCAAACATTTCAATTTACCTGAATCATGTCCTTTT
CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT
GACTGAATTCTTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTTCTGTTCTCTGC
TCTGCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCATCACCATC
10 TTGGATTCTCGCCTCCATACTCCCATGTATTTCTTTCTTGAAACCTCTCATTCTTGACAT
CTGTTACACATCCTCATCCATTCCTCCAATGCTTATTATTTATGTCTGAGAGAAAATCCA
TCTCCTTCATTGGCTGTGCTCTGCAGATGGTTGTGTCCTTGCTGGGCTCCACTGAGTGT
GTCCTCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT
CCATCATCATGAACGGAGTGCTGTATGTGCAAATGGCTGCATGGTCTGGATCATAGGCTG
TCTGACCTCCCTATTGCAAACAGTTCTGACAATGATGTTGCCTTTCTGTGGGAATAATGTC
15 ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAAACCTTGTTTGTTCAGATATCACCAT
CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTCTTCTACTGTTAATTT
TCATCTCCTATGTGTTTATTCTCTCTTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAAG
AAAGCCTTCTCTACCTGTTTCTGAGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT
TTTTATGTACATGAAACCCAAGTCAAAGAACACTAATACATCTGATGAGATTATTGGGCTG
20 TCTTATGGAGTGGTAAGCCCAATGTTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG
TCAAAGAGGCTGTAAAGAAAGTCTGAGCAGACATCTGCATTATTGAAAATGTGA (SEQ
ID NO: 228)

AOLFR124 sequences:

- 25 MNHSVVTEFIILGLTKKPELQGIIFLFLIVYLVAFLGNMLIIAKIYNNTLHTPMYVFLTLAVV
DIICHTSIIPKMLGTMILTSENTISYAGCMSQLFLFTWSLGAEMVLFITMAYDRYVAICFPLHYST
VMNHMCMVALLSMVMALAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPPLALSCSPVRINEV
MVYVADITLAIGDFILTCISYGFIIIVAILRIRTVGKRAKAFSTCSSHLTVVTLYYSPVIYTYIRPASS
YTFERDKVVAALYTLVPTLNPVYSFQNRMQAGIRKVFAFLKH (SEQ ID NO: 229)
- 30 ATGAATCACAGCGTTGTAAGTGAAGTTCATTATTCTGGGCCTCACCAAAAAGCCTGAACTCC
AGGGAATTATCTTCTCTTTTTCTCATTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC
ATCATCATTGCCAAAATCTATAACAACACCTTGACATACGCCCATGTATGTTTCTTCTGAC
ACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT
35 GCTAACATCAGAAAAATACCATTTTATATGCAGGCTGCATGTCCAGCTCTTCTTGTTTACA
TGGTCTCTGGGAGCTGAGATGGTTCTCTTACCACCATGGCCTATGACCGCTATGTGGCCA
TTTGTTCCTCTTCTTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC
ATGGTCAATGGCTATTGCAGTCACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA
CTTTCTGTGGGCCAAACACCATTTGACCACTTCTTCTGTGAGATACCCCATTTGCTGGCTTTG
40 TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCCTGGCCA
TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTTTTATCATTGTTGCTATTCTCCGTATC
CGCACAGTAGAAGGCAAGAGGAAGGCCTTCTCAACATGCTCATCTCATCTCACAGTGGTG
ACCCTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTTGA
AAGAGACAAGGTGGTAGCTGCACTCTATACTCTTGTGACTCCACATTAAACCCGATGGTG
45 TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTTCTGAAA
CACTAG (SEQ ID NO: 230)

AOLFR125 sequences:

- 50 MTNQTQMMFEFLVRFTENWVLLRLHALLFSLIYLTAVLMNLVILLMILDHRLHMAMYFFLRH
LSFLDLCLISATVPKSILNSVASTDSISFLGCVLQLFLVLLAGSEIGILTAMSVDYAAICCPHLC
EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSNLFYGSDELHQFFCDVPALLKLTCSKEHAI
ISVSVAIGVCYAFSCLVCIVSVYVYIFSAVLRISQRQROSKAFSNCVPHLIVVTVFLVTGAVAYL
KPGSDAPSILDLLVSFYSVAPPTLNPVYCLKNKDIKSALS KVLWNVRSSGVMKDD (SEQ ID
NO: 231)

55

WO 01/98526

5 ATGACCAATCAGACACAGATGATGGAATTCTTGCTTGTGAGATTTACTGAGAATTGGGTGC
 TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTA
 GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTTCTCCG
 ACATTTGTCCTTCTTAGACCTGTGTCTCATTTCTGCCACAGTCCCAAATCCATCCTCAACT
 10 CTGTGCGCTCCACTGACTCCATCTCCTTCCTGGGTGTGTGTGCAGCTCTTCTTGGTGGA
 CTGTCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCTATGACCGCTATGTGCCA
 TCTGTGCCCCCTACACTGTGAGGCTGTCTATGAGCAGAGGGCTCTGTGTCCAGTTGATGGC
 AATTTTTATGGCTCTGATGAGCTACATCAGTTCTTCTGCGATGTCCCTGCCCTACTAAAGCT
 15 CACTGTCTCTAAAGAACATGCCATCATTAGTGTGAGTGTGGCCATTGGGGTCTGTTATGCA
 TTTTCATGTTTAGTTTGCATTGTAGTTTCTATGTGTACATTTTCTCTGTGTAAAGGAT
 ATCAGAGACAGAGACAATCCAAAGCCTTTTCCAAGTGTGTGCTCACCTCATTGTTGTC
 ACTGTGTTTCTTGTAAAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT
 TCTAGACTTGTGGTGTCTGTGTTCTATTCTGTGCGACCTCCAACCTGAACCCTGTTATCT
 20 ACTGTCTGAAGAACAAGGACATTAAATCCGCTCTGAGTAAAGTCTGTGGAATGTTAGAA
 GCAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

AOLFR126 sequences:

20 MFLYLCFIFQRTCSEEMEEENATLLTEFVLTGFLHQPDKIPLFLAFLVIYLITMGNLGLVLIW
 KDPHLHIPMYLFLGSLAFVDASLSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL
 ATMAYDRYVAICKALLYPVMITNELCIQLLVLSFIGLLHALIHEAFSRLTFCNSNIQHIFYCDII
 PLLKISCTDSSINFLMVIFAGSVQVFTIGTILISYTHILFTILEKKSIRKAVSTCGAHLVSLSLY
 YGPLTFKYLGSASPQADDQDMMESLFYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID
 NO: 233)

25 ATGTTCTTTACCTTTGCTTCATTTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA
 ATGCAACATTGCTGACAGAGTTTGTCTCACAGGATTTTACATCAACCTGACTGTAAAT
 ACCGCTCTTCTGGCATTCTTGGTAATATATCTCATCACCATCATGGGAATCTTGGTCTAA
 TTGTTCTCATCTGGAAGACCCTCACCTTCATATCCCAATGTACTTATCCTTGGGAGTTA
 30 GCCTTTGTGGATGCTTCGTTATCATCCACAGTGAATGCAATGCTGATCAACTTCTTAG
 CTAAGAGTAAGATGATATCTCTCTGAATGCATGGTACAATTTTTTCCCTGTAAACCAT
 GTAACCACAGAAATGTTTTCTTGGCAACAATGGAATGCAATGCTGATCGCTATGTAGCCATTGCA
 AAGCTTTACTTTATCCAGTCATTATGACCAATGAACTATGCATTGAGCTATTAGCTTGTCA
 TTTATAGGTGGCCTTCTCATGCTTTAATCCATGAAGCTTTTTTCAATCAGATTAACCTTCTG
 35 TAATCCAAACATAATAACAACCTTTACTGTGACATTATCCCATTGTTAAAGATTCTGTGTA
 CTGATTCCTCTATTAACCTTTCTAATGGTTTTTATTTTCGAGGTTCTGTTCAAGTTTACCA
 TTGGAACCTATTCTTATCTTATACAATTATCCTCTTTACAATCTTAGAAAAGAGTCTATC
 AAAGGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATCT
 40 ATGGCCCCCTCACCTTCAAAATCTGGGCTCTGCATCTCCGCAAGCAGATGACCAAGATAT
 GATGGAGTCTCTATTTTACACTGTCTAGTTCTTTATTAATCCCATGATCTACAGCCTGA
 GAAACAAGCAAGTAATAGCTTCATTCACAAAAATGTTCAAAAGCAATGTTTAG (SEQ ID
 NO: 234)

AOLFR127 sequences:

45 MSNEDMEQDNTLLTEFVLTGLTYQPEWKMPFLVFLVIYLTIVWNLGLIALIWNDPQLHIPM
 YFGLGSLAFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY
 VAICKPLLYPVMNNSLCIRLLAFSFLGGFLHALIHEVLIFRLTFCNSNIHHIFYCDIPLFMISCTD
 PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLVSLSLYGPLIF
 MYLRPASQADDQDMIDSVFYTHIPLLNPIIYSLRNKQVIDSFTKMVRNV (SEQ ID NO: 235)

50 ATGTGCAATGAGGACATGGAACAGGATAATACAACATTGCTGACAGAGTTTGTCTCACA
 GGAATTACATATCAGCCAGAGTGGAAAATGCCCTGTCTTGGTGTCTTGGTGATCTATC
 TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACCTCAC
 ATCCCATGTACTTTTTCTTGGGAGTTTAGCCTTTGTTGATGCTTGGATATCTTCCACAGT
 55 AACTCCCAAAATGTTGGTTAATTTCTTGGCAAAAACAGGATGATATCTGTCTGAATGC
 ATGATTCAATTTTTTCTTGGCAACAAT

GGCATATGATCGCTATGTAGCCATATGCAAACCTTTACTATATCCAGTGATTATGAACAAT
 TCACTATGCATACGGCTGTTAGCCTTCTCATTTTATAGGTGGCTTCCTCCATGCCTTAATTCA
 TGAAGTCCTTATATTCAGATTAACTTCTGCAATTCTAACATAATACATCATTTTTACTGTG
 ATATTATACCACTGTTTATGATTTCCTGTACTGACCCTTCTATTAATTTTCTAATGGTTTTTA
 5 TTTTGTCTGGCTCAATTCAGGTATTCACCATTGTGACAGTTCTTAATTCTTACACATTTGCT
 CTTTTCACAATCCTAAAAAGAAGTCTGTTAGAGGCGTAAGGAAAGCCTTTTCCACCTGTG
 GAGCCCATCTCTTATCTGTCTCTTTATATTATGGCCCACTTATCTTCATGTATTTGCGCCCT
 GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATAACAATCATAATTC
 CTTTGCTAAATCCCATTATCTACAGTCTGAGAAATAACAAGTAATAGATTCAATCACAAA
 10 AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

AOLFR128 sequences:

METQNLTVVTEFILLGLTQSQDAQLLVFVLVLFYLIILPGNFIIFTIKSDPGLTAPLYFFLGNLA
 LLDASYSFIVVPRMLVDLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVMADFRIAICRPLHY
 15 STIMNPRACYALSLVLWLGGFHISIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVEL
 LMVSNSSLGSLLCFLGLLASYAVILCRIREHSSEGKSKAISTCTTHIIIFLMFGPAIFIYTCPFQAFP
 ADKVVSLFHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMF (SEQ ID NO: 237)

ATGGAAACACAGAACCTCACAGTGGTGACAGAATTCATTCTTCTTGGTCTGACCCAGTCTC
 20 AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTATCATCCTCCCTGGA
 AATTTCTCATCATTTTCACCATAAAGTCAGACCTGGGCTCACAGCCCCCTCTATTTCTT
 TCTGGGCAACTTGGCCTTACTGGATGCATCCTACTCCTTCAATTGTGGTTCACAGGATGTTG
 GTGGACTTCCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTCAGCTCTTTT
 TCTTGCATTTTCTTGGAGCGGGAGAGATGTTCTCCTCGTTGTGATGGCCTTTGACCGCTAC
 25 ATCGCCATCTGCCGGCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT
 TATCGTTGGTTCTGTGGCTTGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG
 CACTTGCCTTTCTGTGGCCCAAACAGCTCGATAACTTCTTCTGTGATGTTCCACAGGTCAT
 CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCCTG
 CTCAGCCTCCTGTGCTTCTGGCCTTCTGGCCTCCTATGCAGTCATCCTCTGTGCTATAAG
 30 GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCATATTATCATT
 ATATTTCTCATGTTTGGACCTGCTATTTTCATCTACACTTGCCCTTCCAGGCTTTCCCAGC
 TGACAAGGTAGTTTCTCTTTTCCATACTGTATCTTTCTTTGATGAACCCTGTTATTTATA
 CGCTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTG
 CTGA (SEQ ID NO: 238)

35

AOLFR129 sequences:

MALYFSLILHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLFALFSVI
 YVVTVLGNLLIIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT
 QIFLLHLLGGVEMVLLVSMADFVAICKPLHYMTIMNKKVCVLLVVTSWLLGLLHSGFQIPF
 40 AVNLPFCGPNVVDISIFCDLPLVTKLACIDIYFVQVIVANSGLSLSCFILLISYSLILITIKNHSPT
 GQSKARSTLTAHITVILFFGPCIFIYWPFGNHSVDKFLAVFYTIITPILNPIIYTLRNKEMKISMK
 KLWRAFVNSREDT (SEQ ID NO: 239)

ATGGCTCTTTATTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTCTCTCTACAGG
 45 TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAACTATTAAATCAATCTCAAGTGTC
 AGAATTCATTTTGTGGGACTGACCAGCTCCCAGGATGTAGAGTTTCTTCTTTTGGCCTCT
 TCTCGGTTATCTATGTGGTCACAGTTTGGGTAACCTTCTATTATAGTCACAGTGTTTAAAC
 ACCCCTAACCTGAATACTCCCATGTATTTTCTCCTTGGTAATCTCTCTTTGTAGATATGAC
 CCTTGCTTCTTTGCCACCCCTAAGGTGATTCTGAACTTGTTAAAAAGCAGAAGGTAATT
 50 TCTTTTGTGGGTGCTTCACTCAGATATTTCTCCTTCACTTACTGGGTGGGGTTGAAATGGT
 ACTGTTGGTCTCCATGGCTTTTGACAGATATGTGGCCATTTGTAAGCCCTACACTACATG
 ACCATCATGAACAAGAAGGTATGTGTTTGTGTTAGTGACCTCATGGCTCTTGGGTCTCC
 TTCACTCAGGGTTTCAGATACCATTGTGCTGTGAACCTTGCCCTTTTGTGGTCCCAATGTGGTA
 GACAGCATTTTTTGTGACCTCCCTTTGGTTACTAAGCTTGCCCTGTATAGACATATTTTTGT
 55 ACAGGTAGTCATTGTTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTCATTATTTTGTCTA
 TCTCCTACAGTCTGATCCTCATAACCATTAAAGAACCTCTCCTACTGGGCAATCTAAAGC

CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTCTCTTTGGCCCATGCATCTTTA
TCTACATTTGGCCCTTCGGCAACCACTCTGTAGATAAGTTCCTTGCTGTGTTTTATACCATC
ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA
TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

5

AOLFR131 sequences:

MASTSNVTELIIFTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS
LVEISYSSTIAPKFIIDLLAKIKTISLEGCLTQIFFHFHFGVAEILLIVVMAYDCYVAICKPLHYMNI
ISRQLCHLLVAGSWLGGFCHSIIQLVIIQLPFCGPNVIDHYFCDLQPLFLACTDTFMEGVIVLA
10 NSGLFSVFSFLILVSSYIVILVNLNRNHSAGRHKALSTCASHITVVILFFGPAIFLYMRPSSTFTED
KLAVFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

15

ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG
TGCAGAGTGTATGCTTTGTGGTGTCTCCCCGTGTACCTTGCCACGGTGGTGGGCAATGG
CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCCTTA
GCTGCCTGTCTTGGTGGAGATCAGTTATTCTCCACTATCGCCCCATAATTCATCATAGAC
TTACTTGCCAAGATTAACCAATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA
CTTCTTTGGGGTTGTGAGATCCTTTTGATTGTGGTGATGGCCTATGATTGCTACGTGGCC
20 ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTACCTTCTGGTGGC
TGGTTCCTGGCTGGGGGGCTTTTGTACTCCATAATTAGATTCTCGTTATCATCCAATTGC
CCTCTGTGGTCCCAATGTGATTGACCACTATTTCTGTGACCTCCAGCCTTTATTCAAGCTT
GCCTGCACTGACACCTTCATGGAGGGGTTATTGTGTGGCCAACAGTGGATTATTCTCTG
TCTTCTCCTTCCTCATCTTGGTGTCTCTTATATTGTCACTTCTGGTCAACTGAGGAACCAT
TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT
25 TGTTTTTTGGACCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTCACTGAAGATAAA
CTTGTGGCTGATTCTACACGGTCATACCCCCATGCTGAACCCCATCATTTACACACTCAG
GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA
GGGAGTGA (SEQ ID NO: 242)

30

AOLFR132 sequences:

MVATNNVTEIIFVGFSSQNWSEQRVISVMFLMYTAVVLGNGLIVVTILASKVLTSPMYFFLSYL
SFVEICYCSVMAPKLIFDSFIKRVISLKGCLTQMFSLHFFGGTEAFLMVMAYDRYVAICKPL
HYMAINQRMCGLLVRIA WGGGLLHVSQGTFILFQLPFCGPNIMDHYFCDVHPVLELACADT
FFISLLITNGGSISVVSFFVLMASYLIILHFLRSHNLEGQHKALSTCASHVTVVDLFFIPCSLVYR
35 PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

40

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCCAGAATTGGAGTG
AGCAGAGGGTCATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG
CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCCATGTATTTCTTTCTCA
GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTCTATGGCCCCCAAGCTTATCTTTGAC
TCCTTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTTCCCTCC
ATTTCTTTGGTGGCACTGAGGCCTTTCTCCTGATGGTGATGGCCTATGACCGCTATGTGGC
CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG
AGGATAGCATGGGGCGGGGGCTGCTGCATTCTGTTGGGCAAACCTTCTGATTTTCCAGC
45 TCCCGTTCTGTGGCCCCAACATCATGGACCACTACTTCTGTGATGTCCACCCAGTGCTGGA
GCTGGCCTGCGCAGACACCTTCTCATTAGCCTGCTGATCATCACCATGGCGGCTCCATC
TCCGTAGTCAGTTTCTCGTGCTGATGGCTTCTACCTGATCATCTGCATTCTCTGAGAAG
CCACAACCTGGAGGGGCGAGCACAAGGCCCTCTCCACCTGTGCTCCTCATGTACAGTTGTC
GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACCCCTCCCTGCAGA
50 CAAGATAGTTGCTGATTTTATACAGTGGTCACACCTCTCTAAACCTGTGATTTACTCCT
TCAGGAATGCTGAAGTGAAAAATGCCATGAGGAGATTATTGGGGGAAAAGTAATTTGA
(SEQ ID NO: 244)

AOLFR133 sequences:

55

MTEFIFLVSPNQEVQRVCFVIFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS
SATAPKLISDLLAERKVISWWGCMALFLLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN

WQVCTVLVGIAWVGGFMHSFAQILLIFHLLFCGPNVINHYFCDLVPLLKLACSDTFLIGLLIVAN
GGTLSVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI
DKMVAVFYTVITAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

- 5 ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG
TGATATTTCTGTTCTTGACACAGCAATTGTGCTGGGGAATTCCTCATTGTGCTCACTGTC
ATGACCAGCAGAAGCCTTGGTTCCCCCATGTACTTCTTCTCAGCTACCTCTCCTTCATGGA
GATCTGCTACTCCTCCGCTACAGCCCCCAAACCTCATCTCAGATCTGCTGGCTGAAAGGAAA
GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGCACTTCTTTGGTGGCACTGA
10 GATTTTCTGCTCACTGTGATGGCCTATGACCACTATGTGGCCATCTGCAAGCCCCCTCAGC
TACACCACCATCATGAACCTGGCAGGTGTGACTGTCTTGTAGGAATAGCATGGGTGGGA
GGCTTCATGCATTCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTTCTGTGGCCCCAA
TGTGATCAATCACTATTTCTGTGACCTAGTTCCCTTCTCAAACCTGCCTGCTCTGACACCT
TCCTCATTGGTCTGCTGATTGTTGCCAATGGAGGCACCCTGTCTGTGATCAGTTTTGGGGT
15 CCTCTTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG
TGCAAAGCCCTCTCCACCTGTGGGTCCCATTTTCGCTGTGGTTATCTTGTTCTTTGGGCCCTG
CGTCTTCAACTCTCTGAGGCCTTCTACCACTCTGCCCATAGACAAGATGGTGGCTGTGTTCT
ACACAGTGATAACCGCGATCCTGAACCCTGTCATCTACTCTCTGAGAAATGCTGAAATGAG
GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID
20 NO: 246)

AOLFR134 sequences:

- MTTILEVDNHTVTTRFILLGFPTRPAFQLLFFSIFLATYLLTLENLLIILAIHSDGQLHKPMYFFL
SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC
25 NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFLAQLHYCGMPQINHYFCDISPLNVSCE
DASQAEMVDFFLALMVIAIPLCVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSM
LFTYARPKLMYAYNSNKVVSVLTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQGNQAFS
S (SEQ ID NO: 247)

- 30 ATGACCACCATAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTCATTCTTCTGG
GGTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTCTCCATTTTCTGGCAACCTATCTG
CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA
AGCCCATGTACTTCTTCTTGAGCCACCTCTCCTTCTGGAGATGTGGTATGTCACAGTCATC
AGCCCCAAGATGCTTGTGACTTCTCAGTCATGACAAGAGTATTTCTTCAATGGCTGCA
35 TGACTCAACTTTACTTTTTGTGACCTTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG
GCCTTTGACCGCTATGTAGCCATTTGTAATCCACTACGCTACCCAGTCATCATGACCAACC
AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGACTGCCATGATTAA
GATGGTTTTATAGCACAACCTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGTG
ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT
40 CTCTTGCCCTCATGGTCATTGCTATTCTCTTTGTGTTGTGGTGGCATCCTACGCTGCTA
TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG
TGCTCCACCTGACCGTCGTAATTCTCTTATTCCATGACACTTTTACCTATGCCCGTC
CCAAACTCATGTATGCCTACAATTCCAACAAAGTGGTATCTGTTCTTACACTGTCATTGTT
CCACTCCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA
45 AGACCATACATTGCAGAGGAAGTGGGCCCCAGGGAAATGGGGCTTTCAGTAGTTAA (SEQ
ID NO: 248)

AOLFR135 sequences:

- MIFPSHDSQAFTSVDMEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILRT
50 DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL
AAMAYDRHAAICNPLLYSGTMSTALCTGLVAGSYIGGFLNAIAHTANTFRLHFCGKNIDHFFC
DAPPLVKMSCTNTRVYEKVLGTVGFTVLSSILAILISYVNILLAILRIHSASGRHKAFSTCASHL
ISVMLFYGSLLFMYSRPSSTYSLERDKVAALFYTVINPLLNPLIYSLRNKDIKEAFRKATQTIQPO
T (SEQ ID NO: 249)

55

WO 01/98526

5 ATGATTTTCCCTTCTCATGATAGTCAGGCTTTACCTCCGTGGACATGGAAGTGGGAAATT
 GCACCATCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTCCCAGTGGCAGCCGAT
 TCTATTTGGAGTGTCTGATGCTCTATTTGATAACCTTGTGAGGAAACATGACCTTGGTTA
 TCTTAATCCGAAGTATTCCCACTTGCATACACCTATGTACTTTTTTATTGGCAATCTGTCT
 10 TTTTGGATTTCTGGTATACCTCTGTGTATACCCCCAAAATCCTGGCCAGTTGTGTCTCAGA
 AGATAAGCGCATTTCCCTGGCTGGATGTGGGCTCAGCTGTTTTTCTGTGTGTAGCCT
 AACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTTGTAACCC
 ATTGCTTTATTAGGTACCATGTCCACCGCCCTCTGTACTGGGCTTGTGCTGGCTCTACA
 TAGGAGGATTTTTGAATGCCATAGCCATACTGCCAATACATTCCGCTTGCATTTTGTGG
 15 TAAAAATATCATTGACCACTTTTTCTGTGATGCACACCATTGGTAAAAATGCTGTACA
 AACACCAGGGTCTACGAAAAAGTCTGCTTGGTGTGGTGGGCTTACAGTACTCTCCAGCA
 TTCTTGCTATCCTGATTTCTATGTCAACATCCTCCTGGCTATCCTGAGAATCCACTCAGCT
 TCAGGAAGACACAAGGCATTCTCCACTGTGCTTCCCACCTCATCTCAGTCATGCTCTTCTA
 TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTTCCACCTACTCCCTAGAGAGGGACAAA
 20 GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCCCTCTCATCTATAGCCTGAG
 AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG
 A (SEQ ID NO: 250)

AOLFR136 sequences:

20 MTMENYSMAAQFVLDGLTQQAELQLPLFLLFLGIYVTVVGNLGMILLIAVSPLLHTPMYYFL
 SLSFVDFCYSSVITPKMLVNFLGKNTILYSECMVQLFFVVFVAEGYLLTAMAYDRYVAIC
 SPLLYNAIMSSWVCSLLVLAFFLGFSLALHTSAMMKLSFCKSHIINHFCVDLPLNLSCSNT
 HLNELLLFIAGFNTLVPTLAVAVSYAFILYSLHRSSEGRSKAFGTCSHLMVVFIFGSITFMY
 FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

25 ATGACCATGGAAAATTATTCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAAACACAGCAAG
 CAGAGCTCCAGCTGCCCTCTTCCCTCCTGTTCCCTGGGAATCTATGTGGTCACAGTAGTGGG
 CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTACTATT
 TCCTCAGCAGCTTGTCTTCGTCGATTTCTGCTATTCCTCTGTCATTACTCCCAAAATGCTG
 30 GTGAACCTCCTAGGAAAGAAGAATAACAATCCTTTACTCTGAGTGCATGGTCCAGCTTTTT
 TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACTCTGAGTGCATGGTCCAGCTTTTT
 TGTGGCCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCTCATGGGTCTGCTCACTGC
 TAGTGTGGCTGCCTTCTTCTGGGCTTCTCTGCTTGAATGCGATCATGTCTCATGGGTCTGCTCACTGC
 35 AAAGTGTCTTTTGCAAATCCCACATTATCAACCATTAATCTGTGATGTTCTTCCCTCCT
 CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTTATCATTGCGGGGTTTA
 ACACCTTGGTGCCCACTAGCTGTTGCTGCTCCTATGCCTTCATCCTCTACAGCATCCTT
 CACATCCGCTCCTCAGAGGGCCGTCCTCAAGCTTTTGAACATGCAGCTCTCATCTCATGG
 CTGTGGTGATCTTTTGGGTCCATTACCTTCATGATTTCAAGCCCCCTCAAGTAACCTCC
 CTGGACCAGGAGAAGGTGCTCTGTGTTCTACACCACGGTGATCCCCATGCTGAACCTT
 40 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTTAGTAGGAA
 AATGA (SEQ ID NO: 252)

AOLFR137 sequences:

45 MSPENQSSVSEFLLGLPIRPEQQA VFFALFLGMYLTTVLGNLLIMLLIQLDLHSLHTPMYFLLSH
 LALTDISFSSVTPKMLMNMQTQHLAVFYKGCISQTYFFIFFADLDSFLITSMAYDRYVAICPL
 HYATIMTQSQCVMLVAGSWVIACALLHTLLAQLSFCADHIIPHYFCDLGALLKLSCSDTSL
 NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQIPSTKGICKALSTCGSHLSVVTIYRTIIGLYFLP
 PSSNTNDKNIIASVIYTA VTPMLNPFYISLRNKDIKGALRKLLSRGAVAHACNLSTLGG (SEQ
 ID NO: 253)

50 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTCCTGGGCTCCCCATCCGGC
 CAGAGCAGCAGGCCGTGTTCTTCGCCCTGTTCCCTGGGCATGTACCTGACCACGGTGCTGGG
 GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTACTTCT
 TCCTTAGCCACTTGGCCCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
 55 ATGAACATGCAGACTCAGACCTAGCCGTCTTTTACAAGGGATGCATTTACAGACATATT
 TTTTCATATTTTGTGCTGACTTAGACAGTTTCTTCACTTCAATGGCATATGACAGGTAT

GTGGCCATCTGTCATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTGTCATGC
 TGGTGGCTGGGTCCTGGGTCATCGCTTGTGCGTGTGCTCTTTTGCATACCCCTCCTGGCC
 CAGCTTTCCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGCCCTGCT
 CAAGTTGTCCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA
 5 GCCATTATGCTTCCATTCTGTGCATCCTGGTTTCTTATGGTCACATTGGGGTCACCATCCT
 CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGTCCACTTGTGGATCCACCTCTCA
 GTGGTGACTATCTATTATCGGACAATTATTGGTCTCTATTTTCTTCCCCCATCCAGCAACAC
 CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA
 TTCATTTACAGTCTGAGAAATAAAGACATTAAGGGAGCCCTAAGAAAACCTCTTGAGTAGG
 10 TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

AOLFR138 sequences:

MLNFTDVTEFILLGLTSRREWQVLFFIVFLVYIITVVGNI GMMMLLIKVSPQLNSPMYFFLSHLS
 FVDVWFSSNVTPKMLENLFSDKKTISYADCLAQCFFIALVHVEIFILAAIAFDRTYVIGNPLLY
 15 GSKMSRGCIRLITFPYIYGFLTSLTATLWTYGLYFCGKIEINHFCADPPLIKMACAGTFVKEY
 TMLILAGINFTYSLTVIIISYLFILAILMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRPTE
 ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

ATGCTCAATTTACCGATGTGACAGAGTTCAATCTTTTGGGGCTAACGAGCCGTCGGGAAT
 20 GGCAAGTTCTCTTCTTCATCGTTTTTCTTGTGGTCTACATTATCACCGTGGTGGGCAATATC
 GGCATGATGTTGTTAATCAAGGTCAGTCCTCAGCTTAACAGCCCCATGTACTTTTCTCTCA
 GTCACCTGTCAATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAT
 CTGTTATCAGATAAAAAACAATTTCTTATGCTGGCTGTTTAGCACAGTGTCTTCTTCTCAT
 TGCTCTTGTCCATGTGGAAATTTTATCTTGTGCTGCGATTGCCTTTGATAGATACACAGTGA
 25 TTGGAAATCCTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTGCACTGATTAC
 TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT
 ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
 GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGCTCATACTTGCCGGCATCAAACTC
 ACATATTCCCTGACTGTAATTATCATCTCTTACTTATTATCCTCATTTGCCATTCTGCGAAT
 30 GCGCTCAGCAGAAGGAAGGCAGAAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
 CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
 GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
 TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
 GTTAA (SEQ ID NO: 256)

35

AOLFR139 sequences:

MGFPGIHSWQHWSLPLALLYLLALSANILILIIINKEAALHQPMMYYFLGILAMADIGLATTIMP
 KILAILWFNAKTISLLECF AQMYAIHCFVAMESSTFVCMADRYVAICRPLRYPYIITESFVFKAN
 GFMALRNSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLSDDRRINSINQVLLAWTLMGS
 40 DLGLIILSYALILYSVLKLNSPEAASKALSTCTSHLILILFFYTVIIVISITRSTGMRVPLIPVLLNL
 HNVIPPALNPMVYALKNKELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCCTGGCTCTGCTCT
 ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT
 45 GCACCAGCCTATGTACTATTTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC
 ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG
 AGTGCTTTGCTCAGATGTATGCCATACATTGCTTTGTGGCCATGGAATCAAGTACCTTTGT
 CTGCATGGCTATTGATAGATATGTAGCCATTTGTGACCGCTACGATATCCATCAATCATC
 ACTGAATCTTTTGTCTTCAAAGCAAATGGGTTTATGGCACTGAGAAACAGCCTGTGTCTCA
 50 TCTCAGTGCTCTGTTGGCTGCCAGAGGCATTACTGCTCCCAGAAATCAAATTGAGCACTG
 TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATT
 AACCAGGTCCTTTTGGCTTGGACACTCATGGGAAGTGACCTGGGTTTGATTATTTTATCAT
 ATGCTCTAATACTTTACTCTGTCCTGAAGCTGAAGTCTCCAGAAGCTGCATCCAAGGCCTT
 AAGTACCTGCACCTCCACCTCATCTTAATCCTTTTCTTCTACACAGTCATCATTGTGATTT
 55 CCATTACTCGTAGTACAGGAATGAGAGTTCCCTTATTCCAGTTCTACTTAATGTGCTACA

CAATGTCATTCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAGGAACCTCAGG
CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAGGGCACCTGA (SEQ ID NO: 258)

AOLFR140 sequences:

5 MLTLNKTDLIPASFILNGVPGLEDQLWISFPFCSMYVAMVGNCGLLYLIHYEDALHKPMYY
FLAMLSFTDLVMCSSTIPKALCIFWHLKDIGFDECLVQMFHHTFTGMESGVLMLMALDRYV
AICYPLRYSTILTNPVIAKVGATFLRGVLLIIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCG
NVKVNAIYGLMVALLIGGFDILCITISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAF
10 FSFFSHRFGHEHPPSCHIIIVANIYLLLPPTMNPVYGVKTKQIRDCVIRLSGSKDTKSYSM (SEQ
ID NO: 259)

ATGCTAACACTGAATAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCCAG
GACTGGAAGACACAACTCTGGATTTCCTTCCCATTCTGCTCTATGTATGTTGTGGCTAT
GGTAGGGAATTGTGGACTCCTCTACCTCATTCACTATGAGGATGCCCTGCACAAACCCATG
15 TACTACTTCTTGGCCATGCTTTCCTTACTGACCTGTATGTGCTCTAGTACAATCCCTAA
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTGATGAATGCCTGTCCAG
ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG
ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCATCCTGTAATT
20 GCAAAGGTTGGGACTGCCACCTTCCTGAGAGGGGTATTACTCATTATTCCCTTACTTTCT
CACCAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCATACTACTGTGACCACATG
TCTGTAGCCAAATTGTCCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG
CCCTCCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCCGG
GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGGCAGAAGGCCTTTAATACCTGCACTGCCC
ACATTTGTGCCATTGTTTTCTCCTATACTCCAGCTTTCTTCTCCTTTTCCACCGCTTTG
25 GGGAACACATAATCCCCCTTCTTGCCACATCATTGTAGCCAATATTTATCTGCTCCTACCA
CCCACTATGAACCCCTATTGTCTATGGGGTGAAAACCAAACAGATACGAGACTGTGTCATAA
GGATCCTTTCAGGTTCTAAGGATACCAATCCTACAGCATGTGA (SEQ ID NO: 260)

AOLFR141 sequences:

30 MSSTLGHNMESPNHTDVPDSVFFLLGIPGLEQFHLWLSLPVCGLTATIVGNITILVVVATEPVL
HKPVYVFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFHAFMCMESTVLLAM
AFDRYVAICHPLRYATILDTIAHIGVAAVVRGSLMLPCPFLIGRLNFCQSHVILHTYCEHMA
VVKLACGDRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTGSHVC
VILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPALNPVYGVKTKQIRKRVVRVFQSGQ
35 GMGIKASE (SEQ ID NO: 261)

ATGTCCAGCACTCTTGGCCACAACATGGAATCTCCTAATCACAATGATGTTGACCCTTCTG
TCTTCTCCTCCTGGGCATCCCAGGTCTGGAACAATTCATTTGTGGCTCTCACTCCCTGTG
TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTGGCACTG
40 AACCAGTCTTGACACAAGCCTGTGTACCTTTTTCTGTGCATGCTCTCAACCATCGACTGGCT
GCCTCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT
CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTATGCCTTCTGCATGATGGAGTCCACT
GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA
CAATCCTCACTGACACCATCATTGCCACATAGGGGTGGCAGCTGTAGTGCGAGGCTCCCT
45 GCTCATGCTCCCATGTCCCTTCTTATTGGGCGTTTGAACCTTCTGCCAAAGCCATGTGATCC
TACACACGTACTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAGGCCTA
ACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGTTGACTTGTTTTGCATTGG
TCTCTCCTATGCCCTAAGTGACAAGCTGTCCTTCGCCTCTCATCCCATGAAGCTCGGTCCA
AGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATCTTATACACCAGCCCTC
50 TTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTCACATTCTTTTGGC
CAATGTTTATCTGCTTTTGGCACCTGCTCTAATCCTGTGGTATATGGAGTTAAGACCAAAC
AGATCCGTAAAAGAGTTGTCAGGGTGTTCAAAGTGGCAGGGAATGGGCATCAAGGCAT
CTGAGTGA (SEQ ID NO: 262)

AOLFR143 sequences:

MLGLNGTPFPATLQLTGIPGIQTGLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPMYYFL
 SMLALNDLGVSFSTLPTVISTFCFNYNHVAFNACL VQMFFIHTFSFMESGILLAMSLDRFVAICY
 PLRYVTVLTHNRILAMGLGILTKSFTTLFPFPFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI
 5 HVNNIYGLLVIIFTYGMDSFILLSYALILRAMLVISQEQRLKALNTCMSHICAVLAFYVPIIAVS
 MIHRFWKSAPPVVHVMMSNVYLFVPPMLNPIIYSVKTKAIRKGILKFFHKSQA (SEQ ID NO:
 263)

ATGCTGGGTCTCAATGGCACCCCTTCCAGCCAGCAACACTCCAGCTGACAGGCATTCCTG
 10 GGATACAAACAGGCCTCACCTGGGTTGCCCTGATTTTCTGCATCCTCTACATGATCTCCATT
 GTAGGTAACCTCAGCATTCTCACTCTGGTGTTTTGGGAGCCTGCTCTGCATCAGCCCATGT
 ACTACTTCCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCTTTTCTACACTTCCCACT
 GTGATTTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTAATGCTTGCTGGTCCAGAT
 GTTCTTCATCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC
 15 GCTTTGTGGCTATTTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG
 GCTATGGGTCTGGGCATCCTTACCAAGAGTTTCACCACTCTCTCCCTTTCCCTTTTGTGGT
 GAAACGACTGCCCTTCTGCAAAGGCAATGTTTTGCATCACTCCTACTGTCTCCATCCAGAT
 CTGATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA
 TTTTACCTATGGTATGGACTCAACTTTCATCCTGCTTTCCTACGCATTGATCCTGAGAGCC
 20 ATGCTGGTCATCATATCCCAGGAACAGCGGCTCAAGGCACTCAACACCTGCATGTCACACA
 TCTGTGCAGTGCTGGCCTTTTATGTGCCATAATTGCTGTCTCCATGATTCACCGCTTCTGG
 AAAAGTGCTCCACCTGTTGTTTCATGTCATGATGTCCAATGTCTACCTGTTTGTACCACCCAT
 GCTCAACCCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC
 TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)

25

AOLFR144 sequences:

MGLFNVTHPAFFLLTGIPGLESSHWSLGPCLVEMYAVALGGNTVILQAVRVEPSLHEPMMYYFL
 SMLSFSDDVAISMATLPTVLRITFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYVAICD
 PLRYATVLTTEVIAAMGLGAAARSFITLPLPFLIKRLPICRSNVLSHSYCLHPDMMRLACADISI
 30 NSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS
 TVHRFGKHVPCYIHLMSNVYLFVPPVLNPLIYSAKTKEIRRAIFRMFHHIKI (SEQ ID NO: 265)

ATGGGGTTGTTCAATGTCACTCACCTGCATTCTTCTCCTGACTGGTATCCCTGGTCTGGA
 GAGCTCTCACTCCTGGCTGTCAGGGCCCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA
 35 AATACAGTGATCCTGCAGGCTGTGCGAGTGAGGCCAGCCTCCATGAGCCCATGTACTACT
 TCCTGTCCATGTTGTCCTTCAGTGATGTGGCCATATCCATGGCCACACTGCCCACTGTACTC
 CGAACCTTCTGCCTCAATGCCCGCAACATCACTTTTGATGCCTGTCTAATTCAGATGTTTCT
 TATTCACCTTCTTCTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTTGACCGCTATG
 TGGCCATTTGTGACCCCTTGCCTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT
 40 GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCTTTTCCCTCTTCCCTTTCTTATTAAGA
 GGCTGCCTATCTGCAGATCCAATGTTCTTCTCACTCCTACTGCCTGCACCCAGACATGATG
 AGGCTTGCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTTGTTCTTGTATCCAC
 CTTTGGCATGGACCTGTTTTTATCTTCTCTCCTATGTGCTCATTCTGCGTTCTGTCTATGG
 CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTACATATCCTGGC
 45 TGTACTTGCATTTTATGTGCCAATGATTGGGGTCTCCACAGTGCACCGCTTTGGGAAGCAT
 GTCCCATGCTACATACATGTCCTCATGTCAAATGTGTACCTATTTGTGCTCCTGTGCTCAA
 CCCTCTCATTTATAGCGCCAAGACAAAGGAAATCCGCCGAGCCATTTCCGCATGTTTCAC
 CACATCAAAAATATGA (SEQ ID NO: 266)

AOLFR145 sequences:

MSVQYSLSPQFMLLSNITQFSPIFYLTSPFGLGKHWIFIPFFMYMVAISGNCFILIIKTNPRH
 TPMYYLLSLLALDGLCVSTLPTTMGIFWFNSQSIYFACQIQMFCIHSFSFMESSVLLMMSFD
 RFVAICHPLRYSVIITGQQVVRAGLIVFRGPVATIPVLLLKAFPYCGSVVLSHSFCLHQEVIQLA
 5 CTDITFNLYGLMVVFTVMLDLVLIALSGLIHTVAGLASQEEQRRAFQCTAHLCAVLVF
 FVPMMLSLVHRFGKHAPPAIHLMLANVYLFVPPMLNPIIYSIKTKEIHRAIKLLGLKKASK
 (SEQ ID NO: 267)

10 ATGTCAGTCCAATATTCGCTCAGTCCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG
 CCCCATATTCTATCTACCAGCTTTCCTGGATTGGAAGGCATCAAACACTGGATTTCATCC
 CCTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG
 ACCAACCCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT
 GGGGCTGTGTGTCCACGTTGCCACCACTATGGGGATCTTCTGGTTTAACTCCCAGAGT
 ATCTACTTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTCTTCATGGAGTC
 15 CTCAGTGCTCCTCATGATGTCCTTTGACCGCTTTGTGGCCATCTGCCACCCTCTGAGGTATT
 CGGTCAATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTCCGGGGACC
 TGTGGCCACTATCCCTATTGTCCTCCTCCTGAAGGCTTTCCCTACTGTGGATCTGTGGTCC
 TCTCCCACTCATTTTGCCTGCACCAGGAAGTGATACAGCTGGCCTGCACAGATACCACCTT
 CAATAATCTGTATGGACTGATGGTGGTAGTTTTCACTGTGATGCTGGACCTGGTGTCTCATC
 20 GCACTGTCTATGGACTCATCTGCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC
 GCCGTGCCTTTCAGACATGCACCGCTCATCTCTGTGCTGTGCTAGTATTCTTTGTGCCCATG
 ATGGGGCTGTCCCTGGTGCACCGTTTTGGGAAGCATGCCCCACCTGCTATTCTTCTTAT
 GGCCAATGTCTACCTTTTGTGCCTCCCATGCTTAACCCAATCATATACAGCATTAAAGACC
 AAGGAGATCCACCGTGCCATTATCAAACCTCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ
 25 ID NO: 268)

AOLFR146 sequences:

MSQVTNTTQEGIFYLTDIPGFEASHIWISIPVCCLYTISIMGNTTILTVIRTEPSVHQRMVFLSM
 LALDGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFLHGFSFMESSVLLAMSVDCYVAICCP
 30 LHYASILTNEVIGRTGLAIICCVLAVLPSLFLKRLPFCHSHLLRSYCLHQDMIRLVACDIRLN
 SWYGFALALLIIVDPLLVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYPMVGVSM
 HRFKASPLVHVIMANIYLLAPPVMNPIIYSVKNKQIQWGMNLNLSLKNMHSR (SEQ ID NO:
 269)

35 ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG
 GATTTGAGGCCTCCACATCTGGATCTCCATCCCCGTCTGCTGTCTCTACACCATCTCCATC
 ATGGGCAATACCACCATCCTCACTGTCATTGCGACAGAGCCATCTGTCCACAGCGCATGT
 ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCCCTACCACCTACCCACA
 GTCATGCAGCTTCTCTGGTTCAACGTTCTGAGAATCAGCTCTGAGGCCTGTTTGTCTCAGTT
 40 TTTCTTCTTCATGGATTCTCCTTATGGAGTCTTCTGTCTCCTCCTGGCTATGTCCGTTGACT
 GCTATGTGGCCATCTGCTGTCCCTCCATTATGCCTCCATCCTCACCAATGAAGTCATTGGT
 AGAACTGGGTAGCCATCATTTGCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT
 CAAGCGACTGCCTTTCTGCCACTCCACCTTCTCTCTCGCTCCTATTGCCTCCACCAGGATA
 TGATCCGCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTGCTCTTGCTT
 45 GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCCTATACACTATTCTGAAAAATA
 TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCCTGTCCACAT
 TCTAGCTGTCTGGTCTCTACATTCCCATGGTTGGTGTATCTACTGCTGGCAGCCCCGGT
 AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCAGCCCCGGT
 GATGAACCCCATCATTTACAGTGTAAGAACAAGCAGATCCAATGGGGAATGTAAATTC
 50 CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

AOLFR147 sequences:

MPSASAMIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCIIYIVAVVGNCLLYLIVVEHSLHEPMF
 FFLSMLAMTDLILSTAGVPKALSIFWLGAIREITFPGLTQMFFLHYNFVLDLSAILMAMAFDHYV
 55 AICSPRYTTILTPKTIKSAMGISFRSFCILPDVFLLTCLPFCRTRIPTYCEHIGVAQLACADISI
 NFWYGFCVPIMTVISDVILIAVSYAHILCAVFLPSQDACQKALGTCGSHVCVILMFYTPAFFSI

LAHRFGHNVSRTFHIMFANLYIVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO: 271)

5 ATGCCATCTGCCTCTGCCATGATCATTTTCAACCTGAGCAGTTACAATCCAGGACCCCTTCAT
TCTGGTAGGGATCCCAGGCCTGGAGCAATTCATGTGTGGATTGGAATTCCTTCTGTATC
ATCTACATTGTAGCTGTTGTGGGAACTGCATCCTTCTCTACCTCATTGTGGTGGAGCATA
GTCTTCATGAACCCATGTTCTTCTTCTCTCCATGCTGGCCATGACTGACCTCATCTTGTCC
ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTTTGGCTAGGGGCTCGCGAAATCACATTCC
CAGGATGCCTTACACAAATGTTCTTCCCTTCACTATAACTTTGTCCTGGATTGAGCCATTCTG
10 ATGGCCATGGCATTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATAACCACCATCTT
GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTTCGAAGCTTCTGCATCATC
CTGCCAGATGTATTCTTGCTGACATGCCTGCCTTTCTGCAGGACACGCATCATACCCACACA
CATACTGTGAGCATATAGGTGTTGCCAGCTCGCCTGTGCTGATATCTCCATCAACTTCTG
GTATGGCTTTTGTGTTCCCATCATGACGGTCACTCAGATGTGATTCTCATTGCTGTTTCTCCT
15 ACGCACACATCCTCTGTGCTGTCTTGGCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT
CGGCACITGTGGTTCTCATGTCTGTGTCATCCTCATGTTTTATACACCTGCCTTTTCTCCA
TCCTCGCCCATCGCTTGGACACAATGTCTCTCGCACCTTCCACATCATGTTTGCCAATCTC
TACATTGTTATCCACCTGCACTCAACCCCATGGTTTACGGAGTGAAGACCAAGCAGATCA
GAGATAAGGTTATACTTTTGTCTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

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AOLFR148 sequences:

MPTVNHSGTSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFIILTKRSLHEPMYLFLC
MLAGADIVLSTCTIPQALAIWFWRAGDISLDRCITQLFFIHSTFISESGILLVMAFDHYIAICYPLR
YTTILTALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIPHTFCEHIGLAKYACNDIRINIWYG
25 FSILMSTVVLDDVVLIFISYMLILHAVFHMPSPDACHKALNTFGSHVCIILFYGSGIFTILTQRFGR
HIPPCIHIPLANVCILAPPMNLPIIYGIKTKQIQEQVVQFLFIKQKITLV (SEQ ID NO: 273)

ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG
GCCTACAGGACCAGCACATGTGGATTTCTATCCCATTCTTCATTCCCTATGTCACCGCCCTT
30 CTTGGGAACAGCCTGCTCATCTTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT
ACCTCTTCCCTCTGCATGCTGGCTGGAGCAGACATTGTCCTCTCCACGTGCACCATTCCTCAG
GCCTTAGCTATCTTCTGGTTCCGTGCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT
CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGATGGCCTTTGACC
ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATTCCTTACAAATGCTCTGATCAA
35 GAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTTCCCTATCATATTTCTTT
TAAAAAGATTGACTTTCTGCCAGAATAATATTATTCACACACCTTTTGTGAACACATTGG
CCTAGCCAAATATGCATGTAATGACATTGCAATAAACATTTGGTATGGGTTTTCCATTCTA
ATGTCGACGGTGGTCTTAGATGTTGTACTAATTTTTATTTCCCTATATGCTGATTCTCCATGC
TGTCTTCCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTTGGCTCCCATG
40 TCTGCATCATCATCCTCTTTTATGGGTCTGGCATCTTCAACAATCCTTACCCAGAGGTTTGGA
CGCCACATTCACCTTGATCCACATCCCGTTGGCTAATGTCTGCATTCTGGCTCCACCTAT
GCTGAATCCCATTATTTATGGGATCAAACCAAGCAAATCCAGGAACAGGTGGTTCAGTTT
TTGTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

AOLFR149 sequences:

MSNASLLTAFILMGLPHAPALDAPLFGVFLVYVLTVLGNLLILLVIRVDSHLHTTMYFLTNL
SFIDMWFSVTVPKLLMTLVFPSGRAISFHSMAQLYFFHFLGGTECFLYRVMSCDRYLAISSYP
LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWQHYLCDAPPILKLACADTS
AIETVIFVTVGIVASGCFVLIVLSYVSIVCSILRIRTSEKHFRAFQTCASHCIVVLCFFGPGLFIYLR
50 PGSRKAVDGVVAVFYTVLTPLLNPVVYTLRNKEVKKALLKLKDKVAHSQSK (SEQ ID NO:
275)

ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC
TGGACGCCCCCTCTTTGGAGTCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
55 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCTCA
CCAACCTGTCGTTCAATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC

TTTGGTGTTCCTCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTCT
 TTCCTTCTAGGGGGCACCAGTGTTCCTCTACAGGGTCATGCTGTGATCGCTACCT
 GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG
 GCCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGGCCATATTGACTTTCC
 5 ATTTGCCCTACTGTGGACCAACTGGATCCAGCACTATTTGTGTGATGCACCGCCCATCCT
 GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCATTTTTGTGACTGTTGGAATA
 GTGGCCTCGGGCTGCTTTGTCCTGATAGTGTCTCTATGTGTCCATCGTCTGTTCATCCT
 GCGGATCCGCACCTCAGAGGGGAAGCACAGACCTTTCAGACCTGTGCCCTCCACTGTATC
 GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCAATTTACCTGAGGCCAGGCTCCAGGAAAGC
 10 TGTGGATGGAGTTGTGGCCGTTTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGT
 ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC
 ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

AOLFR150 sequences:

15 MELGNVTRVKEFIFLGLTQSQDQSLVLFLLCLVYMTLLGNLLIMVTVTCESSLHTPMYFLLR
 NLAILDICFSSTAPKVLLDLLSKKKTISYTSMTQIFLHLLGGADIFSLSVMAFDCYMAISKPL
 HYVTIMSRGQCTALISASWMGGFVHSIVQISLLLPLFCGPNVLDTFYCDVPQVILKTCTDTFA
 LEFLMISNNGLVTTLWFIFLLVSYTVILMTLSQAGGGRRKAISTCTSPHHCGDPAFCALHLCLC
 PALHCPPHRKGHLCHLHCHLPSAEPFDLHSEEPGNEVSHEKTEEKTRAF (SEQ ID NO: 277)

20 ATGGAGTTGGGAAATGTCACCAGAGTAAAAGAATTTATATTTCTGGGACTTACTCAATCCC
 AAGACCAGAGTTTGGTCTTGTCTTTTTTATGTCTTGTGTACATGACGACTCTGCTGGGA
 AACCTCCTCATCATGGTCACCGTGACCTGTGAGTCTCGCCTTACACCCCCATGTACTTCT
 GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAAGCTGCTCTAAAGTCTTGC
 25 TGGACCTTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT
 CTTCCACCTCCTTGGTGGGGCAGACATTTTTTCTCTCTGTGATGGCGTTTACTGTCTACA
 TGGCCATCTCCAAGCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT
 CATCTCTGCCTCTTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC
 CTCTCCCTTTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCAGGTCTC
 30 AAATCACTTGCACTGACACTTTTGTCTTGTGAGTTCTTGATGATTCCAACAATGGCCTGGT
 CACTACCCTGTGGTTTATCTTCTGCTTGTGTCTTACACAGTCATCCTAATGACGCTGAGGT
 CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTTGCACCTCCCCACATCACTGTG
 GTGACCTGCAATTTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCAC
 AGAAAAGGCCATCTCTGTACCTTCACTGTCTCTCCCTCTGCTGAACCTTTGATCTACA
 35 CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT
 CTGA (SEQ ID NO: 278)

AOLFR151 sequences:

40 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLRTNSHLQTPMYFFLGHLS
 FVDICYSSNVTPNMLHNFLSEQKTISYAGCFTQCLLFIALVITEFYILASMAIDRYVAICSPHYLS
 SRMSKNICVCLVTIPYMYGFLSGFSQSLTFLHLSFCGSLEINHFYCADPPLIMLACSDTRVKKMA
 MFVVAGFNLSSSLFIILLSYLFIFAAIFRIRSAEGRHKAFSTCASHLTIVTLFYGTLCFMYVRPPE
 KSVEESKITAVFYTFLSPMLNPLIYSLRNTDVLAMQQMIRGKSFHKIAV (SEQ ID NO: 279)

45 ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC
 CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCTTGGGATCTACCTAATCACACTGGCAGG
 CAACCTGTGCATGATCCTGCTGATCAGGACCAATCCCACCTGCAAAACCCCATGTATTTC
 TTCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTTACTCCAAATATGCT
 GCACAATTTCTCTCAGAACAAGACCATCTCTACGCTGGATGCTTACACAGTGTCTT
 50 CTCTCATCGCCCTGGTGATCACTGAGTTTTACATCCTTGCTTCAATGGCATTGGATCGCTA
 TGAGCCATTTGCAGCCCTTTGCATTACAGTTCCAGGATGTCCAAGACATCTGTGTCTGT
 CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTCTCTCAGTCACTGCTAACCTT
 TCACTATCCTTCTGTGGTCCCTTGAATCAATCATTTCTACTGCGCTGATCCTCCTCTTA
 TCATGCTGGCCTGCTCTGACACCCGTGTCAAAAAGATGGCAATGTTTGTAGTTGCAGGCTT
 55 TAATCTCTCAAGCTCTCTCTCATCATTTCTGTCTCTATCTTTTCAATTTTGCAGCGATCTT
 CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCTTTTCTACGTGTGCTTCCACCTGACA

ATAGTCACTTTGTTTTATGGAACCCTCTTCTGCATGTACGTAAGGCCTCCATCAGAGAAGT
CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTTATACTTTTTTGAGCCCAATGCTGAACCC
ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA
AAATCCTTTCATAAAATTGCAGTTTAG (SEQ ID NO: 280)

5

AOLFR152 sequences:

MDQINHTNVKEFFLELTRSRELEFFLFVVFFAVYVATVLGNALIVVTITCESRLHTPMYFLLRN
KSVLDIVFSSITVPKFLVDLLSDRK TISYND CMAQIFFFH FAGGADIFFLSVMAYDRYLAIAKPL
HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPFPFCGPNTLDAFYCYVLQVVKLACTDT
10 FALELFMISNGLVTLLWFLLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLHFVPCV
YIYCRPFMTLPMDDTISINNTVITPMLNPIIYSLRNQEMKSAMQRLQRRLLGPSES RKWG (SEQ ID
NO: 281)

ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCTGGAACCTTACACGTTCCC
15 GAGAGCTGGAGTTTTTCTTGTTGTGGTCTTCTTGTCTGTGTATGTAGCAACAGTCCTGGG
AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCCTACACACTCCTATGTACTTTC
TCCTGCGGAACAAATCAGTCCTGGACATCGTTTTTTCATCTATCACCGTCCCCAAGTTCCTG
GTGGATCTTTTATCAGACAGGAAAACCATCTCCTACAATGACTGCATGGCACAGATCTTTT
TCTTCCACTTTGCTGGTGGGGCAGATATTTTTTCTCTCTGTGATGGCCTATGACAGATAC
20 CTTGCAATCGCCAAGCCCTGCACTATGTGACCATGATGAGGAAAGAGGTGTGGGTGGCC
TTGGTGGTGGCTTCTTGGGTGAGTGGTGGTTTGCATTCAATCATCCAGGTAATTCTGATGC
TTCCATTCCCCTTCTGTGGCCCCAACACACTGGATGCCTTCTACTGTTATGTGCTCCAGGTG
GTAAACTGGCCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTCTAACAACGGAC
TGGTGACCCTGCTCTGGTTCTCTGCTCCTGGGCTCCTACACTGTCATTCTGGTGATGCTG
25 AGATCCCACTCTGGGGAGGGGCGGAACAAGGCCCTCTCCACGTGCACGTCCCACATGCTG
GTGGTGA CTCTTCACTTCGTGCCTTGTGTTTACATCTACTGCCGGCCCTTCATGACGCTGCC
CATGGACACAACCATATCCATTAAATAACACGGTCATTACCCCCATGCTGAACCCCATCATC
TATTCCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG
CCTTCCGAGAGCAGAAAATGGGGGTGA (SEQ ID NO: 282)

30

AOLFR153 sequences:

MSKTSLVTA FILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMTLVSPSGRAISFHS CVAQLYFFHFLGSTECFLYTVMSYDRYLAI SYPL
RYTSMMSGSRCALLATSTWLSGSLHSAVQ TILTFHLPYCGPNQIQHYLCDAPPILKLACADTSA
35 NEMVIFVDIGLVASGCFL LIVLSYVSIVCSILRIHTSEGRHRAFQTCASHCIVVL CFFVXCVFIYLR
PGSRDVVDGVVAIFYTVLTPLLNPVYVTLRNKEVKKAVLKL RDKVAHSQGE (SEQ ID NO:
283)

ATGTCCAAGACCAGCCTCGTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
40 TGGACGCCCCACTCTTTGGAATCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
TCCACTTCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCCTATGATCGCTACTTG
45 GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGATGTGCCCTCCTGG
CCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTATTTGTGTGATGCACCGCCCATCCTGA
AACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGGACATTGGGCTAGT
GGCCTCGGGCTGCTTCTCCTGATAGTGCTGTCTTATGTGTCCATCGTCTGTTCCATCCTGC
50 GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGCATCGT
GGTCTTTTGCTTTTTTGTNNCCTGTGTTTTCATTTACCTGAGACCAGGCTCCAGGGACGTCG
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT
TCTCAGGGAGAATAA (SEQ ID NO: 284)

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WO 01/98526

AOLFR156 sequences:

MCWAMPSPFTGSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLFIYTFIHDNLLIFS AVR L
 DTHLGNPMYNFISFISFLEI WYT TATIPKMLS NLISEKKAISMTGCILQMYFFHSLENSEGILLTT
 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGFLILLPEIVMISTLPFCGPNQIHQIFCDLVP
 5 VLSLACTDTSMLIEDVIHAVTHITFLIALSYVRIVTVILRIPSSEGRQKAXSTCAGHLMVFLIFG
 SVSLMYLRFSNTYPPVLDTAIALMFTVLAPFFNPIIYSLRNKDMNNAIKKLFCLQKVLNKP GG
 (SEQ ID NO: 285)

10 ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA
 ACCAATCAACAGTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT
 CCTGTACTTCTTTCCTTACTTTTCTATCTATACTTTTATTATCATTGATAACTTATTAATCTT
 CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT
 CCTTCTGGAGATCTGGTACACCACAGCCACCATCCCAAGATGCTCTCCAACCTCATCAG
 TGAAAAGAAGGCCATCTCAATGACTGGCTGCATCTTGCAGATGTATTTCTTCCACTCACTT
 15 GAAAACTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA
 ACCCTCTTCGCTATCAAATGATCATGACCCCCCGGCTCTGTGCTCACCTCTCTGCAGGTTCC
 TGCCTCTTCGGTTTCCTTATCCTGCTTCCCGAGATTGTGATGATTTCCACACTGCCTTTCTG
 TGGGCCCAACCAAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT
 ACAGACACGTCCATGATTCTGATTGAGGATGTGATTGCTGTGACCATCATCATTACCT
 20 TCCTAATCATTGCCCTGTCTATGTAAGAATTGTCACTGTGATAATTGAGGATTCCTTCTT
 GAAGGGAGGCAAAAAGGCTNTTCTACCTGTGCAGGCCACCTCATGGTCTTCTGTATTTCT
 TTGGCAGTGTATCACTCATGTACTTGCCTTTCAGCAACACTTATCCACCAGTTTGGACAC
 AGCCATTGCACTGATGTTTACTGTACTTGCCTTCTCAATCCCATCATTTATAGCCTGA
 GAAACAAGGACATGAACAATGCAATTA AAAA AACTGTTCTGTCTTCAAAAAGTGTGAACA
 25 AGCCTGGAGGTAA (SEQ ID NO: 286)

AOLFR157 sequences:

MAMDNVTA VFQFL LIGISNYPQWRDTFFTLVLIYLS TLLGNGFMIFLIHFDPNLHTPIYFFLSNL
 SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP
 30 LRYSVVMNGPVCVCLVATSWGTSVL TAMLILSLRLHFCGANVINHFACEILSLIKLTCSDTSL
 NEFMILITSIFTLLL PFGFVLLSYIRIAMAIIRSLQGR LKAFTTCGSHLTVVTIFYGSAISM MYMKT
 QSKSSPDQDKFISVFY GALTPMLNPLIYSLRKKDV KRAIRK VMLKRT (SEQ ID NO: 287)

35 ATGGCCATGGACAATGTACAGCAGTGTTCAGTTTCTCCTTATTGGCATTCTTA ACTATCC
 TCAATGGAGAGACAGTTTTTTACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG
 AATGGATTTATGATCTTTCTTACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT
 CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG
 TGCATTGTTTCTCTACCCATCCCTACCTCTCTATCCCCGATGTTTGGCTCAAACGAGTGTG
 TCCTTGGCTTTGGCCACAGCAGAGTGCCTCTACTGGCTGCCATGGCCTATGACCGTGTGG
 40 TTGCTATCAGCAATCCCTGCGTTATTCAGTGGTTATGAATGGCCAGTGTGTGTCTGCTT
 GGTGCTACCTCATGGGGACATCACTTGTGCTCACTGCTCATCCTATCCCTGAGG
 CTTCACTTCTGTGGGCTAATGTCATCAACCATTTTGCCTGTGAGATTCTCTCCCTCATTA
 GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAGTATCTTCAACC
 TGCTGCTACCATTTGGGTTTGTCTCCTCTCCTACATACGAATTGCTATGGCTATCATAAGG
 45 ATTCGCTCACTCCAGGCAGGCTCAAGGCCTTTACCACATGTGGCTCTCACCTGACCGTGG
 TGACAATCTTCTATGGGTCAGCCATCTCCATGTATATGAAA ACTCAGTCCAAGTCTCCCC
 ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG
 ACATGA (SEQ ID NO: 288)

50

AOLFR158 sequences:

MKAGNFSDTPEFFLLGLSGDPELQPIFLF LMYLATMLGNLLIILAVNSDSLHTPMYFLLSI
 LSLVDICFTSTTMPKMLVNIQAQASINYTGCLTQICFVLV FVGLENGILVMMAYDRFVAICHP
 LRYNVIMNPKLCGLLLLLSFIVSVLDALLHTLMVLQ LTFCIDLEPHFFCEL AHILKLACSDVLIN
 55 NILVYLVTSL LGVPLSGHFSYTRIVSSVMKIPSAGGKYKAFSICGSHLIVVSLFYGTGFGVYLS
 GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKDM LKALRKLISRIPSFH (SEQ ID NO: 289)

ATGAAAGCAGGAACTTCTCAGACACTCCAGAATTCTTTCTCTTGGGATTGTCAGGGGATC
 CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCTGTCCATGTACCTGGCCACAATGCTGGG
 GAACCTGCTCATCATCCTGGCCGTCAACTCTGACTCCCACCTCCACACCCCCATGTACTTCC
 5 TCCTCTCTATCCTGTCTTGGTCGACATCTGTTTACCTCCACCACGATGCCCAAGATGCTG
 GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTCACCCAAATCTGCT
 TTGTCTGGTTTTTGTGGATTGGAAAATGGAATTCTGGTCATGATGGCCTATGATCGATT
 TGTGGCCATCTGTCACCCACTGAGGTACAATGTCATCATGAACCCCAAATCTGTGGGCTG
 CTGCTTCTGCTGTCCTTCATCGTTAGTGTCTGCTGCTGCTGCACACGTTGATGGTGCT
 10 ACAGCTGACCTTCTGCATAGACCTGGAAATTCCTTCTGTGAACTAGCTCATATTC
 TCAAGCTCGCCTGTTCTGATGTCCTCATCAATAACATCCTGGTGTATTTGGTGACCAGCCT
 GTTAGGTGTTGTTCTCTCTCTGGGATCATTTTCTCTTACACACGAATTGTCTCTCTGTCA
 TGAATAATCCATCAGCTGGTGGAAAGTATAAAGCTTTTCCATCTGCGGGTACACATTTAAT
 CGTTGTTTCTTGTGTTTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT
 15 CCTCCAGGAAGGGTGCAATAGCATCAGTGATGTATACCGTGGTCACCCCATGCTGAACCC
 ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAACTAATATCTAG
 GATACCATCTTTCCATTGA (SEQ ID NO: 290)

AOLFR159 sequences:

20 MGPRNQTA VSEFLMKVTEDPELKLIPFSLFLSMYLVITLGNLLILLAVISDSHLHTPMYFLLFN
 LSFTDICLTTTTVPKILVNIQAQNSITYTGCLTQICLVLFAGLESCFLAVMAYDRYVAICHPL
 RYTVLMNVHFWGLLILLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKLACSDTL
 INNILIYFASSVFGAIPLSGIIFSYSQIVTSVLRMPARGKYKAFSTCGCHLSVFSLFYGTAFGVYIS
 SAVAESSRITAVASVMYTVVPQMMNPFYSLRNKEMKKALKLIGRLFPF (SEQ ID NO: 291)

25 ATGGGACCCAGAAACCAAACAGCTGTTTCAGAATTTCTTCTCATGAAAGTGACAGAGGAC
 CCAGAACTGAAGTTAATCCCTTTCAGCCTGTTCTGTCCATGTACCTGGTCACCATCCTGG
 GGAACCTGCTCATTCTCCTGGCTGTCATCTCTGACTCCCACCTCCACACCCCCATGTACTTC
 CTTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAAACACAACCACAGTCCCAAAGATCCT
 30 AGTGAACATCCAAGCTCAGAATCAGAGTACTTACACAGGCTGCCTCACCCAGATCTGT
 CTTGTCTTGGTTTTTGTGCTGGCTTGAAAGTTGCTTTCTTGCAGTCATGGCCTACGACCGCTA
 TGTGGCCATTTGCCACCCACTGAGGTACACAGTCCTCATGAATGTCCATTTCTGGGGCTTG
 CTGATTCTTCTCTCCATGTTTCATGAGCACTATGGATGCCCTGGTTTCAGAGTCTGATGGTATT
 GCAGCTGTCCTTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTACGGTC
 35 ATCAAGCTCGCCTGTTCTGACACCCTCATCAACAACATCCTCATATATTTTGCAAGTAGTGT
 ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTCTTATTCTCAAATAGTCACCTCTGTTT
 TGAGAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACCTGTGGCTGTCACCTCTC
 TGTTTTTCTTGTCTATGGGACAGCTTTTGGGGTGTACATTAGTTCTGCTGTTGCTGAGT
 CTTCCCGAATTACTGCTGTGGCTTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC
 40 CTTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAACTTATTGGTAG
 GCTGTTTCCTTTTAG (SEQ ID NO: 292)

AOLFR160 sequences:

45 MPMQLLLDFIIFSIRFIINSMEARNQTAISKFLLGLIEDPELQPVLFSLFLSMYLVITLGNLLILL
 AVISDSHLHTPMYFFLSNLSFLDICLSTTTIPKMLVNIQAQNSITYSGCLTQICFVLFAGLENC
 LLAAMAYDRYVAICHPLRYTVIMNPRLCGLLILLSLLTSVNNALLLSLMVLRSLFCTDLEIPLFF
 CELAQVIQLTCSDTLINNILIYFAACIFGGVPLSGIILSYTQITSCVLRMPASGKHKA VSTCGSHL
 SIVLLFYGAGLGVISSVVTDSPRKTA VASVMYSVFPQMVNPFYSLRNKDMKGTLRKFIGRIP
 SLLWCAICFGFRFLE (SEQ ID NO: 293)

50 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG
 CATGGAAGCGAGAAACCAAACAGCTATTTCAAAATTCCTTCTCCTGGGACTGATAGAGGAT
 CCGGAACCTGCAGCCCGTCTTTTTAGCCTGTTCTGTCCATGTACTTGGTCACCATCCTGGG
 GAACCTGCTCATCCTCTTGGCTGTCATCTCTGACTCTCACCTCCACACCCCCATGTACTTCT
 55 TCCTCTCCAATCTCTCCTTTTTGGACATTTGTTTAAGCACAACCACGATCCCAAAGATGCTG
 GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCTCACCCAGATCTGCT

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TTGTCTTGT TTTTGTGCTGGCTTGGAAAATTGTCTCCTTGCAGCAATGGCCTATGACCGCTAT
 GTGGCCATTTGTACCCCTTAGATACACAGTCATGAACCCCGCCTCTGTGGCCTGC
 TGATCTTCTCTCTGTGACTAGTGTGTGAATGCCCTTCTTCTCAGCCTGATGGTGTG
 AGGCTGTCTTCTGCACAGACCTGGAAATCCCGCTCTTCTTCTGTGAAGTGGCTCAGGTCA
 5 TCCAACTCACCTGTTGACACCCCTCATCAATAACATCCTGATATATTTTGCAGCTTGCATA
 TTTGGTGGTGTCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTT
 GAGAATGCCATCAGCAAGTGGAAGCACAAGCAGTTCCACCTGTGGGTCTCACCTCTCC
 ATTGTCTCTTGTCTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTTACTGACTC
 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTTCCCTCAAATGGTGAACCCC
 10 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTCATAGGGAGG
 ATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTGAGGTTTCTAGAGTAA (SEQ ID
 NO: 294)

AOLFR161 sequences:

15 MEPRNQTSASQFILLGLSEKPEQETLLFSLFFCMYLVMMVGNLLILAISIDSHLHTPMYFFLANL
 SLVDFCLATNTIPKMLVSLQTGSKAISYPCLIQMYFFHFFGIVDSVIHAMMAYDRFVAICHPLH
 YAKIMSLRLCRLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR
 IFILIVAGMVIATPFVCILASYARILVAIMKVPSAGGRKKAFTSCSSHLSVVALFYGTIGVYLCP
 SSVLTTVKEKASAVMYTAVTPMLNPFYSLNRDLKGALRKL VNRKITSSS (SEQ ID NO: 295)

20 ATGGAACCAAGAAACCAAACCAAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC
 CAGAGCAGGAGACGCTTCTCTTTCCCTGTTCTTCTGCATGTACCTGGTCATGGTCGTGGG
 GAACCTGCTCATCATCCTGGCCATCAGCATAGACTCCACCTCCACACCCCATGTACTTCT
 TCCTGGCCAACCTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT
 25 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC
 TTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGT
 CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTGCGCTG
 CTGGTCGGCGCCCTCTGGGCGTTTTCTGCTTCATCTCACTCACTCACATCCTCCTGATGGC
 CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC
 30 TCCGACTTTCGTGCACGGACACCTCTGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT
 GGTGATAGCCACGCCCTTGTCTGCATCCTGGCCTCCTATGCTCGCATCCTGTGGCCATCA
 TGAAGGTCCCCTCTGCAGGCGGCAGGAAGAAAGCCTTCTCCACCTGCAGTCCACCTGTC
 TGTGGTTGCTCTTCTATGGGACCACCATTTGGCGTCTATCTGTGTCCCTCCTCGGTCTCA
 CCACTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCAACCCCATGCTGAATCC
 35 CTTCTATACAGCTTGAGGAACAGAGACCTGAAAGGGCTCTCAGGAAGCTGGTCAACAG
 AAAGATCACCTCATCTTCTCTGA (SEQ ID NO: 296)

AOLFR162 sequences:

40 MMRLMKEVRGRNQTEVTEFLLGLSDNPDQGVLFALFLIYMANMVGNLGMIVLIKIDLCLH
 TPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFGSFLGTECFLLAMMA
 YDRYAAIWNPLLYPVLVSGRICFLIATSFLAGCGNAAIHTGMTFRLSFCGSNRNHFYCDTPPL
 LKLSGSDTHFNGIVIMAFSSFIVISCMIVLISYLCIFIAVLKMPSEGRHKAFSTCASYLMAVTIF
 FGILFMYLRPTSSYSMEQDKVVSFYTIVIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID
 NO: 297)

45 ATGATGAGACTTATGAAAGAGGTTGAGGCAGAAATCAAACAGAAAGTAACAGAATTTCTC
 CTCTTAGGACTTTCCGACAATCCAGATCTACAAGGAGTCTCTTTCATTTGTTTCTGTTGAT
 CTATATGGCAAACATGGTGGGCAATTTGGGGATGATTGTATTGATTAGATTGATCTCTGT
 CTCCACACCCCATGTATTTCTTCTCAGTAGCCTCTCTTTGTAGATGCCTCTTACTCTTCT
 50 TCCGTCACTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG
 GATGTGCTGCCCAGTTCTACTTCTTTGGCTCCTTCTGGGGACTGAGTGCTTCTCTGTTGCTGT
 ATGATGGCATATGACCGCTATGCAGCCATTGGAACCCCTGCTCTACCCAGTTCTCGTGT
 CTGGGAGAATTTGCTTTTGTCTAATAGCTACCTCCTTCTAGCAGTTGTGGAAATGCAGC
 CATAACACAGGGATGACTTTTAGGTTGTCTTTTGTGGTTCTAATAGGATCAACCATTTCT
 55 ACTGTGACACCCCGCCACTGCTCAAACCTCTTGTCTGTATACCCACTTCAATGGCATTGTG
 ATCATGGCATTCTCAAGTTTATTGTATCATGCTGTGTTATGATTGTCTCATTCTCTACCT

GTGTATCTTCATTGCCGTCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAGCCTTCTCC
 ACCTGTGCCTCTTACCTCATGGCTGTCACCATATTCTTTGGAACAATCCTCTTCATGTACTT
 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTCTGTCTTTTATACAGTA
 ATAATCCCTGTGCTAAATCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCC
 5 TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

AOLFR163 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVVFLGVYSLTVVGNSTLIVLICNDSCLHTPMYFFTGN
 10 LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL
 LYAQAMSIKLCALLVAVSYCGGFINSIIKKTFSFNFCRENIIDDFCDLLPLVELACGEKGGYK
 IMMYFLLASNVICPAVLILASYLFIITSVLRISSSKGYLKAFTSCSSHLTSVTLYYGSILYIYALPRS
 SYSFDMDKIVSTFYTVVFPMLNLMYSLRNKDVKEALKKLLP (SEQ ID NO: 299)

ATGCAGAGGAGCAATCATACAGTGACTGAGTTTATACTGCTGGGCTTCACCACAGACCCA
 15 GGAATGCAGCTGGGCCTCTTCGTGGTGTTCCTGGGCGTGTACTCTCTCACTGTGGTAGGAA
 ATAGACCCCTCATCGTGTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC
 ACTGGAAATCTGTCTGTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAAGATCCTAGT
 GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCACTTCTTCTTCT
 CTGCAGGGCTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT
 20 GGCCATCTCCAAGCCCCTGCTTTATGCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG
 GTAGCAGTCTCATATTGTGGTGGCTTTATTAACCTCTTCAATCATCACCAGAAAACGTTTTC
 CTTTAACTTCTGCCGTGAAAACATCATTGATGACTTTTTCTGTGATTTGCTTCCCTTGGTGG
 AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTTCTGCTGGCCTCCAA
 TGTCATCTGCCCCGCAGTGCTCATCTGGCCTCCTACCTCTTTATCATCACCAGTGTCTTGA
 25 GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCCACCTGACCTCT
 GTCACTTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCAGATCTAGCTATTCTTT
 TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATCCCCATGTTGAATCTCATG
 ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAATTCTCCCATAA (SEQ
 ID NO: 300)

30

AOLFR164 sequences:

MFLTERNTTSEATFTLLGFSDYLELQIPLFFVFLAVYGFSVVGNLGMIVIIKINPKLHTPMYFFLN
 HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFFCTFVVTELILFAVMAYDHFVAICNP
 35 LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSALKLSFHGFNTINHHFCELSLISLSPDSYL
 SQLLLFTVATFNEISTLLIILTSYAFIIVTTLKMPSASGHRKVFSTCASHLTAITIFHGTLFLYCV
 NSKNRHTVKVASVFYTVVIPLNPLIYSLRNKDVKDAIRKIINTKYFHIKHRHWYPNFVIEQ
 (SEQ ID NO: 301)

ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACCTCTCTTGGGCTTCTCAG
 40 ATTACCTGGAAGTCAAATTCCTCTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG
 GTAGGGAATCTTGGGATGATAGTGATCATCAAATTAACCCAAAATTGCATACCCCCATGT
 ATTTTTCTCCTCAACCACCTCTCCTTTGTGGATTTCTGCTATTCTCCTCCATCATTGCTCCCATGA
 TGCTGGTGAACCTGGTTGTAGAAGATAGAACCATTTCATTCTCAGGATGTTTGGTGCAATT
 CTTTTCTTTTGCACCTTTGTAGTGACTGAATTAATTCTATTGCGGTGATGGCCTATGACC
 45 ACTTTGTGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCCAGAACTCTGTGCC
 ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG
 CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTTCTTCTGTGAGTTATCCTCC
 CTGATATCACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTTCTTTTCACTGTTGCCAC
 TTTAATGAGATAAGCACACTACTCATCTTCTGACATCTTATGCATTTCATCATTTGTCACCA
 50 CCTGAAGATGCCTTCAGCCAGTGGGCACCGCAAAGTCTTCTCCACCTGTGCCTCCCACCT
 GACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTCTACTGTGTACCCAACTCCAAAA
 ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCTTGTGAA
 TCCCCTGATCTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT
 ACAAATATTTTCATATTAAACATAGGCATTGGTATCCATTTAATTTGTTATTGAACAATA
 55 A (SEQ ID NO: 302)

AOLFR165 sequences:

MAVGRNNTIVTKFILLGLSDHPQMKIFLMLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL
 SNLSFLDICYVSSSTAPKMLSIDIETEQTISFVGCATQYFVFCGMGLTECFLLAAMAYDRYAAICN
 PLYTVLISHTLCLKMVVGAYVGGFLSSFIETYSVYQHDFCGPYMINHFFCDLPPVLALSCSDTF
 5 TSEVVTFIVSVVVGIVSVLVVLISYGYIVAADVVKISSATGRTKAFSTCASHLTAVTLFYGSGFFM
 YMRPSSSYSLNRDKVVSIFYALVIPVNPPIYSFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG
 (SEQ ID NO: 303)

10 ATGGCTGTAGGAAGGAACAACACAATTGTGACAAAATTCATTCTCCTGGGACTTTCAGACC
 ATCCTCAAATGAAGATTTTCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC
 TGGAACTTAAGCCTCATTGCCCTCATTAGATGGACTCTCACCTGCACATGCCCATGTACT
 TCTTCTCAGTAACCTGTCCTTCCTGGACATCTGCTATGTGTCTCCACCGCCCTAAGATG
 CTGTCTGACATCATCACAGAGCAGAAAACCATTTCTTTGTTGGCTGTGCCACTCAGTACT
 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG
 15 GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCTCATATCCCATACACTTTGTTTAA
 AGATGGTGGTTGGCGCCTATGTGGGTGGATTCTTAGTTCTTTTATTGAAACATACTCTGT
 CTATCAGCATGATTTCTGTGGGCCCTATATGATCAACCACTTTTTCTGTGACCTCCCTCCAG
 TCCTGGCTCTGTCTGCTCTGATACCTTACCAGCGAGGTGGTGACCTTCATAGTCAGTGT
 GTCGTGGAATAGTGTCTGTGCTAGTGGTCTCATCTCTTATGGTTACATTGTTGCTGCTGT
 20 TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTTCAGCACTTGTGCCTCTCACCTG
 ACTGCTGTGACCCTCTTCTATGGTTCTGGATTCTTCATGTACATGCGACCCAGTTCAGCTA
 CTCCTAAACAGGGACAAGGTGGTGTCCATATTCTATGCCTTGGTGATCCCCGTGGTGAAT
 CCCATCATCTACAGTTTATAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGAA
 AGGGACCCCGGATTTCTCACGGTGGACCATTCTTTTATGACCTTGGGCTAA (SEQ ID
 25 NO: 304)

AOLFR166 sequences:

MEMENCTRVKEFIFLGLTQNVSLVLFLLLVYVTTLLGNLLIMVTVTCESSLHTPMYFLLH
 NLSIADICFSSITVPKVLVDLLSERKTISFNHCFQMFLFHLIGGVDVFSLSVMALDRYVAISKPL
 30 HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLLPLFCGPNVLDTFYCDVHRVLKLAHTDIFIL
 ELLMISNGLLTTLWFFLLVSYIVILSLPKSQAGEGRRKAISTCTSHITVTVLHFVPCIVYVARP
 FTALPMDKAISVTFVISPLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

35 ATGGAGATGGAAAAGTGCACCAGGGTAAAAGAATTTATTTTCTTGGCCTGACCCAGAATC
 GGGAAAGTGAGCTTAGTCTTATTTCTTCTACTCTTGGTGTATGTGACAACTTTGCTGGGA
 AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTT
 GCTCCATAATTTATCTATTGCCGATATCTGCTTCTTCCATCACAGTGCCCAAGGTTCTGG
 TGGACCTTCTGTCTGAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA
 TTCCACCTTATTGGAGGGTGGATGTATTTTCTTCTTTCGGTGATGGCATTGGATCGATATG
 40 TGGCCATCTCCAAGCCCCTGCACTATGCGACTATCATGAGTAGAGACCATTGCATTGGGCT
 CACAGTGGCTGCCTGGTTGGGGGGCTTTGTCCACTCCATCGTGAGATTTCCTGTTGCTC
 CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCT
 CAAACTGGCCCATACAGACATTTTCACTTGAACCTACTAATGATTTCCAACAATGGACTG
 CTCACCACACTGTGGTTTTTCTGCTCCTGGTGTCTTACATAGTCATATTATCATTACCCAA
 45 GTCTCAGGCAGGAGAGGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACTGT
 GGTGACCCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCCGGCCCTTCACTGCCCTCCCA
 TGGATAAGGCCATCTCTGTACCTTCACTGTCTCTCCCTCTGCTCAACCCCTTGATCTAC
 ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT
 TCTGATAGAAAATAG *SEQ ID NO: 306)

50

AOLFR167 sequences:

MSITKAWNSSSVTMFILLGFTDHPQLQALLFVTFGLGIYLLTLAWNLAFLIRGDTHLHTPMYFF
 LSNLSFIDICYSSAVAPNMLTDFWEQKTISFVGCAAQFFFFVGMGLSECLLLTAMAYDRYAAI
 SSPLLYPTIMTQGLCTRMVVGAYVGGFLSSLIQASSIFRLHFCGPNINHFFCDLPPVLALSCSDT
 55 FLSQVVNFLVVVTVGGTSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTLFGTAL

FVYLRPSSSYLLGRDKVVSFVYSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID NO: 307)

5 ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCCTGGGATTCA
CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCCTGGGCATCTATCTTACCACC
CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA
TGTACTTCTTCCTAAGCAACTTATCTTTTCATTGACATCTGCTACTCTTCTGCTGTGGCTCCC
AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTTGTGGGCTGTGCTGCTC
10 AGTTTTTTTTCTTTGTCGGCATGGGTCTGTCTGAGTGCCTCCTCCTGACTGCTATGGCATA
GACCGATATGCAGCCATCTCCAGCCCCCTTCTACCCCACTATCATGACCCAGGGCCTCT
GTACACGCATGGTGGTTGGGGCATATGTTGGTGGCTTCCTGAGCTCCCTGATCCAGGCCAG
CTCCATATTTAGGCTTCACTTTTTCGGACCCAACATCATCAACCACTTCTTCTGCGACCTCC
CACCAGTCTGGCTCTGTCTTGCTCTGACACCTTCCTCAGTCAAGTGGTGAATTTCTCGTG
15 GTGGTCACTGTGCGAGGAACATCGTTCTCCAACCTCCTTATCTCCTATGGTTACATAGTGT
CTGCGGTCCTGAAGATCCCTTCAGCAGAGGGCCGATGGAAAGCCTGCAACACGTGTGCCT
CGCATCTGATGGTGGTGAATCTGTCTGTTTGGGACAGCCCTTTTCGTGTAATTTGCGACCCAG
CTCCAGCTACTTGCTAGGCAGGGACAAGGTGGTGTCTGTTTTCTATTGATTGGTGTATCCCC
ATGCTGAACCTCTCATTTACAGTTTGAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG
GTGTTGGAAGGAAGAAAGTGTTCCTTAG (SEQ ID NO: 308)

20

AOLFR168 sequences:

MEKINNVTETIFWGLSQSPEIEKVCFVVSFFYIIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV
DICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAYDRYVAICKPLHYM
TIMNRETCKNMLLGTWVGFLHSIIQVALVQLPFCGPNEIDHYFCDVHPVLKLACTETIYIG
25 VVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFFGPCTFMYMRPD
TTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO:
309)

30 ATGGAAAAATAAACAACGTAACCTGAATTCATTTTCTGGGGTCTTTCTCAGAGCCCAGAGA
TTGAGAAAGTTTGTGGTGTTCCTTCTTCTACATAATCATTCTTCTGGGAAATCTC
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAGTCACCCATGTATTTCTTCTCAG
CTTCTTGTCTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC
TGTTAGCAAAGGACAAAACCATCTCCTIATGTGGGGTGCATGTTGCAACTGCTTGGAGTAC
35 ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATGTGGCT
ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT
TAGGGACGTGGGTAGGTGGGTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAACCT
ACCTTTTGTGGACCCAATGAGATAGATCACTACTTTTGTGATGTTACCCCTGTGTTGAAA
CTTGCCCTGCACAGAAACATAACATTGTTGGTGTGTTGTGACAGCCAACAGTGGTACCATTG
40 CTCTGGGGAGTTTGTATCTTGCTAATCTCCTACAGCATCATCCTAGTTTCCCTGAGAAAG
CAGTCAGCAGAAGGCAGGCGCAAGCCCTCTCCACCTGTGGCTCCACATTGCCATGGTTCG
TTATCTTTTTTCGGCCCTGTACTTTTATGTACATCGCCCTGATACGACCTTTTCAGAGGAT
AAGATGGTGGCTGTATTTTACACCATTATCACTCCCATGTTAAATCCTCTGATTTATACACT
GAGAAATGCAGAAGTAAAGAATGCAATGAAGAACTGTGGGGCAGAAATGTTTTCTTGGA
45 GGCTAAAGGGAAATAG (SEQ ID NO: 310)

45

AOLFR169 sequences:

MMDNHSSATEFHLLGFGSQGLHHILFAIFFFFYLVTLMGNTVIIVIVCVDKRLQSPMYFFLSHL
STLEILVTTHVPMMLWGLLFLGCRQYLSLHVSINFSCGTMEFALLGVMAVDYVAVCNPLRY
NIIMNSSTCIWVIVSWVFGFLSEIWPIYATFQFTFRKSNSLDHFYCDRGQLKLSCDNTLLTEFI
50 LFLMAVFILIGSLIPTIVSYTYIISTILKIPSASGRRKAFSTFASHFTCVVIGYGSCLFLYVKPKQQT
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLLKD (SEQ ID NO: 311)

55 ATGATGGACAACCACTCTAGTGCCACTGAATTCACCTTCTAGGCTTCCCTGGGTCCCAAG
GACTACACCACATTCTTTTGTCTATATTCTTTTCTTCTATTTAGTGACATTAATGGGAAAC
ACGGTCATCATTGTGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCCT
CAGCCACCTCTCTACCCTGGAGATCCTGGTCACAACCATAATTGTCCCCATGATGCTTTGG

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GGATTGCTCTTCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCCTG
 TGGGACCATGGAGTTTGCATTACTTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTG
 AACCCTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT
 CATGGGTGTTTGGATTCTTTCTGAAATCTGGCCCATCTATGCCACATTTACGTTTACCTTC
 5 CGCAAATCAAATTCATTAGACCAATTTTACTGTGACCGAGGGCAATTGCTCAAACGTGCTC
 GCGATAACACTCTTCTCACAGAGTTTATCCTTTTCTTAATGGCTGTTTTTATTCTCATTGGT
 TCTTTGATCCCTACGATTGTCTCCTACACCTACATTATCTCCACCATCCTCAAGATCCCGTC
 AGCCTCTGGCCGGAGGAAAGCCTTCTCCACTTTTGCCTCCCACTTCACCTGTGTGTGATTG
 GCTATGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACACAGGGAGTTGAGTACAA
 10 TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCTTCTGAATCCTTTCATCTTTACTCT
 TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT
 GAAAGATTAG (SEQ ID NO: 312)

AOLFR170 sequences:

15 MSFTSLIPSLCFSLTLPFLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVVPVSSVSSSMVLCYLSV
 ASPSVFCFSCMQGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTIIHVMVI
 ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMSDLLVPHKVITFTGCMVQFYHFSLGSTSFLIL
 TDMALDRFVAICHPLRYGTLMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH
 FFCDNEPLLQLSCSDTRLLEFWDFLMALTFVLSSFLVTLISYGYVTTVLRIPSASSCQKAFSTCG
 20 SHLTLVFIGYSSTIFLYVRPGKAHSVQVRKVVALVTSVLTLPFLNPFLTFCNQTVKTVLQGMQ
 RLKGLCKAQ (SEQ ID NO: 313)

ATGTCTTTCACTTCTCTCATACCCTCACTCTGTTTCTCCTTGACTCTCCCATTCCTGTTTGT
 TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTGCTTT
 25 CTCTCTCTATTCTCTGTCTGTCCCTGTTTCTTCTGTTTCAAGTTCAATGGTCTCTGTCTC
 TATCTCTCTGTTTCTGCTCTCCGTCTGTCTTTGTTTCTCTTGATGCAGGGCCCCATACTG
 TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCCTCTTGGGCTTCTCCTCTTTGG
 TGAGCTGCAGGCCCTTCTGTATGGCCCTTCTCATGCTTTATCTTCTCGCCTCATGGGAA
 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTC
 30 CTGGGCAATTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGCCAGGTCTACTTC
 CAGACCTGTTGGTCCCCCAAAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC
 CACTTTTCCCTGGGGTCCACCTCCTTCTCATCTGATGAGCCGGGCTATGTGTGTCCAGCTG
 GGCCATCTGCCACCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGTCCAGCTG
 GCTGGGGCTGCCTGGGCAGCTCCTTCTAGCCATGGTACCACTGTCTCTCCCGAGCTC
 35 ATCTTGATTACTGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAATGAACCTTGCCT
 CAGTTGTCATGCTCTGACACTCGCCTGTTGGAATTCTGGGACTTCTGATGGCCTTGACCT
 TGCTCTCAGCTCCTTCTGGTGACCCTCATCTCCTATGGCTACATAGTGACCACTGTGCTGC
 GGATCCCTCTGCCAGCAGCTGCCAGAAGGCTTTCTCCACTTGGCGGTCTCACCTCACACT
 GGTCTTCATCGGCTACAGTAGTACCATTTCTGTATGTACAGGCTGGCAAAGCTCACTCT
 40 GTGCAAGTCAGGAAGGTCGTGGCCTTGGTGACTTCAGTTCTACCCCTTCTCAATCCCT
 TTATCCTTACCTTCTGCAATCAGACAGTTAAAACAGTGCTACAGGGGCAGATGCAGAGGCT
 GAAAGGCCTTGTCAAGGCACAATGA (SEQ ID NO: 314)

AOLFR171 sequences:

45 MVGNLLIWVTTIGSPSLGSLMYFFLAYLSLMDAIYSTAMSPKLMIDLLCDKIAISLSACMGQLFI
 EHLLGGAEVFLVVMAYDRYVAISKPLHYLNIMNRLVCILLVVMAGGFVHSVQIVFLYSLP
 ICGPNVIDHSVCDMYLLELLCLDIFYGLTVVANGGIICMVFTFLLISCGVILNFKTYSQBER
 HKALPTCISHIIVVALVFPCIFMYVRPVSNFPFDKLMTVFYIITLMNPLIYSLRQSEMKNAM
 KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)

50 ATGGTGGGAAACCTCCTCATTGTTGGGTGACTACTATTGGCAGCCCTCCTTGGGCTCCCTAA
 TGTACTTCTTCTTGCCTACTTGTACATTATGGATGCCATATATCCACTGCCATGTACCCC
 AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTCTTGTGAGCTTGCATGGGTC
 AGCTCTTCATAGAACAATTACTTGGTGGTGCAGAGGTCTTCTTTGGTGGTGATGGCCTA
 55 TGATCGCTATGTGGCTATCTTAAGCCGCTGCACTATTTGAACATCATGAATCGACTGGTT
 TGCATCCTTCTGTTGGTGGTGGCCATGATTGGAGGTTTGTGCACTCTGTGTTCAAATGTG

CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT
 ACCCATTGTTGGAAGTGTGTGCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA
 TGGTGGAATAATTTGTATGGTCATCTTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA
 ACTTCCTTAAAACTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA
 5 CATCATTGTGGTTGCCCTCGTTTTTGTTCCTGTATTTTTATGTATGTTAGACCCGTTTCCA
 ACTTTCCCTTTGATAAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT
 TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA
 AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCCACTGAACATATTTATTCCTAGTTCTA
 AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

10

AOLFR172 sequences:

MAETLQLNSTFLHPNFFILTGFPLGSAQTWLTTLVFGPIYLLALLGNGALPAVVWIDSTLHQPM
 FLLAILAATDLGLATSIAPGLLAVLWLGPRSPYAVCLVQMFFVHALTAMESGVLLAMACDR
 AAAIGRPLHYPVLVTKACVGYAALALALKAVAIVVPFLLVAKFEHFQAKTIGHTYCAHMAV
 15 VELVVGNTQATNLYGLALSLAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSSSHICVIL
 AFYIPGLFSYLAHRFGHHTVPKPVHILLSNIYLLLPPALNPLIYGARTKQIRDRLLETFTFRKSPL
 (SEQ ID NO: 317)

ATGGCAGAACTCTACAACCTCAATTCCACCTTCCTACACCCAACTTCTTCATACTGACTG
 20 GCTTTCCAGGGCTAGGAAGTGCCGAGCTTGGCTGACACTGGTCTTTGGGCCCATTTATCT
 GCTGGCCCTGCTGGGCAATGGAGCACTGCCGGCAGTGGTGTGGATAGACTCCACACTGCA
 CCAGCCCATGTTTCTACTGTTGGCCATCCTGGCAGCCACAGACCTGGGCTTAGCCACATCT
 ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCGATCTGTGCCATATGCTGTGT
 GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC
 25 CATGGCCTGTGATCGTGCTGCGGCAATAGGGCGTCCACTGCACTACCCTGTCTGGTCACC
 AAAGCCTGTGTGGGTTATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC
 CTTTCCCACTGCTGGTGGCAAAGTTTGAGCACTTCCAAGCCAAGACCATAGGCCATACCTA
 TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACACAGGCCACCAACTTATA
 TGGTCTGGCACTTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT
 30 GGACTCATTGCCCATGCTGTGCTGCAGCTACCTACCCGGGAGGCCCATGCCAAGGCCTTTG
 GTACATGTAGTTCTCACATCTGTGTCACTTCTGGCCTTCTACATACCTGGTCTCTTCTCCTAC
 CTCGCACACCGCTTTGGTCATCACACTGTCCCAAAGCCTGTGCACATCCTTCTCTCCAACAT
 CTAATTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCGCACCAAGCAGATC
 AGAGACCGACTCCTGGAAACCTTCACATTCAGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

35

AOLFR173 sequences:

MSHTNVITIFHPAVFVLPGIPGLEAYHIWLSIPLCLIIYITAVLGNSILIVVIVMERNLHVPMYFFLS
 MLAVMDILLSTTTVPKALAIFWLQAHNIAFDACVTQGGFFVHMMFVGESAILLAMAFDRFVAIC
 APLRYTTVLTWPVVGRIALAVITRSFCIIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV
 40 NIWYGFSVPVIMVILDVILIAVSYSILRAVFRPLPSQDARHKALSTCGSHLCVILMFYVPSFFTLL
 THHFGRNIPQHVHILLANLYVAVPPMLNPIVYGVKTKQIREGV AHRFFDIKTWCCTSP LGS
 (SEQ ID NO: 319)

ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCTTCCTGGCATCCCTGG
 45 GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTGCCTCATTACATCACTGCAGTCC
 TGGGAAACAGCATCCTGATAGTGGTTATTGTCATGGAACGTAACCTTCATGTGCCCATGTA
 TTTCTTCCTCTCAATGCTGGCCGTCATGGACATCCTGCTGTCTACCACCACTGTGCCCAAGG
 CCTAGCCATCTTTTGGCTTCAAGCACATAACATTGCTTTTGATGCCTGTGTACCCCAAGGC
 TTCTTTGTCCATATGATGTTTGTGGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG
 50 CTTTGTGGCCATTTGTGCCCCACTGAGATATACAACAGTGCTAACATGGCCTGTTGTGGGG
 AGGATTGCTCTGGCCGTCATACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT
 GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTCCCTCACTCCTACTGTGAGCATATTGGA
 GTGGCTCGTTTAGCCTGTGCTGACATCACTGTAAACATTTGGTATGGCTTCTCAGTGCCCAT
 TGCATGGTCATCTTGGATGTTATCCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG
 55 TGTTTCGTTTGGCCTCCAGGATGCTCGGCACAAGGCCCTCAGCACTTGTGGCTCCCACT
 CTGTGTCATCCTTATGTTTTATGTTCCATCCTTCTTACCTTATTGACCCATCATTTTGGGCG

WO 01/98526

TAATATTCCTCAACATGTCCATATCTTGCTGGCCAATCTTTATGTGGCAGTGCCACCAATGC
TGAACCCCATTTGTCTATGGTGTGAAGACTAAGCAGATACGTGAGGGTGTAGCCACCGGT
CTTTGACATCAAGACTTGGTGTGTACCTCCCCTCTGGGCTCATGA (SEQ ID NO: 320)

5 AOLFR175 sequences:

MHFLSQNDLNINLPHLCLHRHSVIAGAFTIHRHMKIFNSPNSSTFTGFILLGFPCPREGQILLFV
LFTVVYLLTLMGNGSIICAVHWDQRLHAPMYILLANFSFLEICYVTSTVPSMLANFLSDTKIISF
SGCFLQFYFFFSLGSTECFFLAVMAFDRLAICRPLRYPTIMTRRLCTNLVNCWVLGFIWFLPI
VNISQMSFCGSRIDHFLCDPAPLLTLTCKKGPVIELVFSVLSPLVFMLFLFIVGSYALVVRVAVL
10 RVPSAAGRRKAFSTCGSHLAVVSLFYGSVLVVMYGSPSKNEAGKQKTVTLFYSVVTPLLPVI
YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAAATGATTTAAATATAAATCTGATTCCCCATCTATGTTTGCACCG
TCATTAGTAATTGCTGGTGTCTTTACAATTCACAGGCACATGAAAATCTTCAACAGCCCC
15 AGCAACTCCAGCACCTTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC
AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTACCTCCTGACCCTCATGGGCAATGGTTCC
ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA
ACTTCTCCTTCTTGGAGATATGTTATGTACCTCCACAGTCCCCAGCATGCTGGCCAACTTC
CTCTCTGACACCAAGATCATCTCGTCTCTGGCTGCTTCCCTCAGTTCTACTTTTCTTCTCC
20 TTGGGCTCTACAGAATGCTTTTTCTGGCAGTTATGGCATTGATCGATACCTTGCCATCTG
TCGGCCTCTACGCTATCCAACATTATGACCAGACGTCTCTGTACCAATCTTGTGGTCAATT
GCTGGGTACTTGGTTTCATCTGGTTCTTGATTCTATCGTCAACATCTCCAAATGTCCTTC
TGTGGATCTAGGATTATTGACCACTTCTATGTGACCCAGCTCCTCTTCTAACTCTCACTTG
CAAAAAAGGCCCTGTGATAGAGCTTGTCTTTCTGTCTTAAGTCTCTGCCTGTCTTTATGC
25 TCTTTCTCTTCAATTGTGGGGTCTATGCTCTGGTCTGAGAGCTGTGTTGAGGGTCCCTTCA
GCAGCTGGGAGAAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCCAACATCTAAGAATGAAGCTGGAAAGC
AGAAGACTGTGACTCTGTTTTATTCTGTTGTTACCCCACTGCTTAACCCTGTGATATATAGT
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTGGGGAACATAA (SEQ ID NO:
30 322)

AOLFR176 sequences:

MFFIIHSLVTSVFLTALGPQNRMTMHFVTEFVLLGFHGQREMQSCFFSFILVLYLLTLLGNGAIVC
AVKLDRLHTPMYILLGNFAFLEIWIYSTVPMNLVNLSEIKTISFSGCFLQFYFFFSLGTECF
35 LSVMAFYDRYLAICRPLHYPSIMTGKFCIILVCVCWVGGLCYVPVIVLISQLPFCGPNIDHLVCD
PGPLFALACISAPSTELICYTFNSMIIFGPPLSILGSYTLVIRAVLCIPSGAGRTKAFSTCGSHLMV
VSLFYGTLMVMYVSPSTSGNPAGMQKIITLVYAMTPFLNPLIYSLRNKMDKALKRVLGLTVS
QN (SEQ ID NO: 323)

ATGTTCTTTATTATTATTCTTTGGTTACTTCTGTTTTCTAACAGCTTTGGGACCCAGAA
CAGAACAATGCATTTTGTGACTGAGTTTGTCTCCTGGGTTTCCATGGTCAAAGGGAGATG
CAGAGCTGCTTCTTCTCATTATCCTGGTTCTCTATCTCCTGACACTGCTAGGGAATGGAGC
TATTGTCTGTGAGTGAATTTGGACAGGCGCTCCACACACCCATGTACATCCTTCTGGGA
AACTTTGCCCTTTCTAGAGATCTGGTACATTTCTCCACTGTCCCAACATGCTAGTCAATAT
45 CCTCTCTGAGATTAACCATCTCCTTCTCTGGTTGCTTCTGCAATTTCTATTTCTTTTTTC
ACTGGGTACAACAGAGTGTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT
ATGCTGGGTAGGCGGATTTCTGTCTATCCAGTCCCTATTGTTCTTATCTCCCAACTCCCT
TCTGTGGGCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCATGTTTGCAGTGGC
50 CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG
GGCCCTTCTCTCCATCTTGGGATCTTACACTCTGGTTCATCAGAGCTGTGCTTGTATTCCC
TCTGGTGTGTCGAACTAAAGCTTTCTCCACATGTGGGTCCCACTAATGGTGGTGTCTC
TATTCTATGGAACCTTATGGTGTATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCTTATCTAT
55 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCTGGGGTTAACAGTTAGC
CAAAACTGA (SEQ ID NO: 324)

AOLFR177 sequences:

- MSFFVVDLRPMNRSATHIVTEFILLGFPWCWKIQIFLFLSLFLVIYVLTLLGNGAIYAVRCNPLLH
 TPMYFLLGNFAFLIWIYVSSSTIPNMLNVNLSKTKAISFSGCFLQFYFFSLGTTECLFLAVMAYD
 5 RYLAICHPLQYPAIMTVRFCGKLVSCWLIGFLGYPIPIFYISQLPFCGPNIIDHFLCDMDPLMAL
 SCAPAPITECIFYTQSSLVLFFTSMYILRSYILLTAVFQVPSAAGRRAKAFSTCGSHLVVVSFLFYG
 TVMVMYVSPTYGIPTLLQKILTLVYSVTTPLFNPLIYTLRNKDMKLALRNVLFGMRIQRNS
 (SEQ ID NO: 325)
- 10 ATGTCTTTCTTCTTTGTAGACTTAAGACCCATGAACAGGTCAGCAACACACATCGTGACAG
 AGTTTATTCTCCTGGGATTCCCTGGTTGCTGGAAGATTGAGATTTTCTCTTCTCATTGTTT
 TTGGTGATTTATGTCTTGACCTTGCTGGGAAATGGAGCCATCATCTATGCAGTGAGATGCA
 ACCCACTACTACACACCCCCATGTACTTTCTGCTGGGAAATTTGCTTCTCTTGAGATCTGG
 TATGTGTCCTCCACTATTCCTAACATGCTAGTCAACATTCTCTCCAAGACCAAGGCCATCTC
 15 ATTTTCTGGGTGCTTCTCTCCAGTTCTATTTCTTCTTTTCACTGGGAACAACCTGAATGTCTCT
 TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCCTGC
 CATCATGACTGTAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTTGGCTTATTGGATTCTTG
 GATACCCAATTCCCATTTTCTACATCTCCCAACTCCCCTTCTGTGGTCTAATATCATTGAT
 CACTTCTGTGTGACATGGACCCATTGATGGCTCTATCCTGTGCCCCAGCTCCCATAACTG
 20 AATGTATTTTCTATACTCAGAGCTCCCTTGCTCTTTTCACTAGTATGTACATTCTTCGA
 TCCTATATCTGTTACTAACAGCTCCCTTGCTCTTTTCACTAGTATGTACATTCTTCGA
 CCTTCTCTACCTGTGGTTCTCATTTGGTTGTGGTATCTCTTTTCTATGGGACAGTCATGGTA
 ATGTATGTAAGTCCTACATATGGGATCCCAACTTTATTGCAGAAGATCCTCACACTGGTAT
 ATTCAGTAACGACTCCTCTTTTAAATCCTCTGATCTATACTCTTCGTAATAAGGACATGAAA
 25 CTCGCTCTGAGAAATGTCCTGTTTGAATGAGAATTCGTCAAATTCGTGA (SEQ ID NO:
 326)

AOLFR178 sequences:

- MVGANHSVVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLILLTVTSDPHLHSPMYFLL
 30 ANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCIQIFFIHVIGGVEMVLLIAMAFDRYVAICKP
 LQYLTIMSPRMCMFFLVAAWVTGLIHSVVLVFNLPFCGPNVSDSFYCDLPRFIKLACTDSY
 RLEFMVTANSFISLGSFFILIISYVVIILTVLKHSSAGLSKALSTLSAHVSVVVLFFGPLIFVYTW
 PSPSHLDKFLAIFDAVLTPVLNPIIYTFRN (SEQ ID NO: 327)
- 35 ATGGTTGGGGCAAATCACTCCGTGGTGTGAGAGTTTGTGTTCTCTGGGACTCACCAATTCCT
 GGGAGATCCGACTTCTCCTCCTTGTTTCTCCTCCATGTTTTACATGGCCAGTATGATGGGA
 AACTCTCTCATTTTGCTCACTGTGACTTCTGACCCTCACTTGCACTCCCCCATGTATTTCT
 GTTAGCCAACCTCTCCTTCATTGACCTGGGTGTTTCTCTGTCACTTCTCCCAAAATGATTT
 ATGACCTGTTGAGAAAGCACGAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAATCTTCTT
 40 CATCCACGTCATTGGCGGTGTGGAGATGGTGTCTCATAGCCATGGCCTTTGACAGATAT
 GTGGCCATATGTAAGCCCCTCCAGTACCTGACCATTATGAGCCCAAGAATGTGCATGTTCT
 TCTTAGTGGCTGCCTGGGTGACCGGCCTTATCCACTCTGTAGTTCAATTGGTTTTTGTAGTA
 AACTTGCCCTTCTGTGGTCTAATGTATCGGACAGCTTTTACTGTGACCTTCTCGGTTTCAT
 CAAACTTGCCTGCACAGACAGCTACCGACTGGAGTTCATGGTTACAGCCAACAGTGGATTC
 45 ATCTCTCTGGGCTCCTTCTTCATACTGATCATTTTCTATGTGGTCATCATTTCTCACTGTTCT
 GAAACACTCTTCAGCTGGTTTATCCAAGGCTCTGTCCACCCTTTCAGCTCACGTCAGTGTG
 GTAGTTTTGTCTTTGGTCTTTGATTTTTGTCTATACGTGGCCATCTCCCTCCACACACCT
 GGATAAGTTTCTGGCCATCTTTGATGCAGTTCTCACTCCTGTTTTAAATCCTATCATCTACA
 CATTGAGGAATTGA (SEQ ID NO: 328)
- 50

AOLFR179 sequences:

- MNGMNHSVVSEFVFMGLTNSREIQLLLVFSLLFYFASMMGNLVIVFTVTMDAHLHSPMYFLL
 ANLSIIDMAFCSITAPKMICDIFKKHKAISFRGCITQIFFSHALGGTEMVLLIAMAFDRYMAICKP
 LHYLTIMSPRMCLYFLATSSIIHLIHSVLVLFVVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEL
 55 EFMVTVNSGLISVGSFVLLVISYIFLFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFFYTW
 PSPTSHLDKYLAIFDAFITPFLNPVIYTFRNKDMKVAMRRLCSRLAHFTKIL (SEQ ID NO: 329)

5 ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTCATGGGACTCACCAACTCAC
 GGGAGATTGAGCTTCTACTTTTTGTTTTCTCTTTGTTGTTCTACTTTGCGAGCATGATGGGA
 AACCTTGTCAATTGTATTCAGTGAACCATGGATGCTCATCTGCACTCCCCCATGTATTTCT
 CCTGGCTAACCTCTCAATCATTGATATGGCATTGCTCAATTACAGCCCCAAGATGATT
 10 GTGATATTTTCAAGAAGCACAAGGCCATCTCCTTTCGGGGATGTATTACTCAGATCTTCTT
 TAGCCATGCTCTTGGGGGCACTGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATA
 ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAATGTGTCTATACT
 TTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTGTGGTA
 GATTTACCTTTTTGTGGTCCTAATATCTTTGACAGTTTTTACTGTGATCTCCCTCGGCTCCT
 CAGACTTGCTGTACCAACACCCAAGAACTGGAGTTCATGGTCACTGTCAATAGTGGACT
 ATTTCTGTGGGCTCCTTTGTCTGTGTAATTTCTTACATCTTCACTGTTCTGTTG
 GAAACATTCTTCTGGTGGTCTAGCCAAGGCCCTCTTACCCTGTCAGCTCATGTCACTGTG
 15 GTCATCTTGTCTTTGGGCCACTGATGTTTTCTACACATGGCCTTCTCCACATCACACCT
 GGATAAATATCTTGCTATTTTGTGATGATTTATTACTCTTTTCTGAATCCAGTTATCTACA
 CATTGAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCAGTCTGCGCATT
 TTACAAAGATTTTGTA (SEQ ID NO: 330)

AOLFR180 sequences:

20 MTNKMAYIYIKNLNYFSFLIVQCLQPTMAIFNNTSSSSNFLTAFPGLECAHVWISIPVCCLYTI
 ALLGNSMIFLVIITKRRLHKPMYYFLSMLAAVDLCLTITLPTVLGVLWFHAREISFKACFIQMF
 FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILTDRMVLVIGLVICIRPAVFLPLLVAINTVSF
 HGGHELSHPFCHYHPEVIKYTYSKPWISSFWGLFLQLYLNGTDVLFILFSYVLILRTVLGIVARKK
 25 QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLPPVLNPIIYSLKTKTIR
 QAMFQLQSKGSWGFNVRGLRGRWD (SEQ ID NO: 331)

30 ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTCTTTCTCCTCATAGT
 TCAGTGCTTCAACCAACCATGGCAATATCAATAACACCACTTCGTCTTCTCAAACCTTCC
 TCCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT
 CTCTACACCATGGCCTCTTGGGAAACAGTATGATCTTTCTTGTCTCATTACTAAGCGGA
 GACTCCACAAACCCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC
 ATTACGACCTTCCCACTGTGCTTGGTGTCTCTGGTTTCATGCCCCGGGAGATCAGCTTTAA
 AGCTTGCTTCATTCAAATGTTCTTTGTGTCATGCTTTCTCCTTGCTGGAGTCTCGGTGCTGG
 35 TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCCACTGAACTATGCTACTATCCTC
 ACAGACAGGATGGTCTGCTGATAGGGCTGGTTCATGTTTTCATGGGGGTCACGAGCTTTCCCATCCA
 TTCCCCTTCTGTAGCCATAAACAATGTGCTTTTCTGTAACCCACTGAACTATGCTACTATCCTC
 TTTTGCTACCAACCCAGAAGTGATCAAATACACATATCCAAACCTTGGATCAGCAGTTTTT
 GGGGACTGTTTCTTCACTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTCTCCTAT
 GTCCTGATCCTCCGTACTGTTCTGGGCATTGTGGCCGAAAGAAGCAACAAAAGCTCTCA
 40 GCATTGTGTCTGTCACATCTGTGCACTGCTATTTTCTATGTGCCACTGATCAGCCTCTCT
 TTGGCACACCGCTCTTCCACTCCACCCCAAGGGTGTCTGTAGCACTTTGGCCAATATTTA
 TCTGCTCTTACCACCTGTGCTGAACCCTATCTTACAGCTTGAAGACCAAGACAATCCGC
 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGTTCATGGGGTTTTAATGTGAGGGGTCTTA
 GGGGAAGATGGGATTGA (SEQ ID NO: 332)

45

AOLFR181 sequences:

MSVLNNSEVKLFLLIGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIKTEPSLHEPMMYYFLAML
 AVSDMGLSLSSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAHNPLR
 YSSILTSNRVAKMGLILAIRSILLVIPFPTLRLKYCQKNLLSHSYCLHQDTMKLACSDNKTNV
 50 IYGFIALCTMLDLALIVLSYVLILKTILSIASLAERLKALNTCVSHICAVLTFYVPIITLAAMHHF
 AKHKSPLVILIADMFLLVPPLMNPVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

55 ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCTTCTGATTGGGATCCCAGGACTGG
 AACATGCCACATTTGGTTCTCCATCCCCATTTGCCTCATGTACCTGCTTGCCATCATGGGC
 AACTGCACCATTTCTTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATTT
 CCTTGCCATGTTGGCTGTCTCTGACATGGGCTGTCCCTCTCCTCCCTTCTACCATGTGTA

GGGTCTTCTTGTTCAATGCCATGGGAATTTACCTAATGCCTGCTTTGCTCAAGAATTCTTC
 ATTCATGGATTCACTGTCATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTTCT
 TGCCATTACAAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAATG
 GGACTTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTTCCCTTCACCTTAAGGAG
 5 ATAAAAATATTGTCAAAAAGAATCTTCTTTCTCACTCATACTGTCTTCATCAGGATACCATGA
 AGCTGGCCTGCTCTGACAACAAGACCAATGTCATCTATGGCTTCTTCATTGCTCTCTGTACT
 ATGCTGGACTTGGCACTGATTGTTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT
 TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGTCTCCCACATCTGTGCTGTG
 CTCACCTTCTATGTGCCCATCATCACCTGGCTGCCATGCATCACTTTGCCAAGCACAAAA
 10 GCCCTCTTGTTGTGATCCTTATTGCAGATATGTTCTTGTTGGTGCCGCCCTTATGAACCCC
 ATTGTGTAAGTGTGTAAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT
 GTATGTGGGAGATAA (SEQ ID NO: 334)

AOLFR182 sequences:

15 MTLGSLGNSSSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIKTERSLHEPMYLFL
 SMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFFIHCFSFLESSVLLSMAFDRFVAICHP
 LHYVSILTNTVIGRIGLVSLGRSVLIFPLPFMLKRFPYCGSPVLSHSYCLHQEVMKLACADMK
 ANSIYGMFVIVSTVGIDSLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV
 IHRFGKQAPHLVQVVMGFMVLLFPPVMNPVYSVKTKQIRDRVTHAFY (SEQ ID NO: 335)

20 ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCCTGCTGAGTG
 GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCCTGTGCTTCATGTATCT
 GGTTTCCATCCCGGGCAACTGCACAATTCTTTTATCATTAAAAACAGAGCGCTCACTTCAT
 GAACCTATGTATCTCTTCCCTGTCCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC
 25 TCTCCCTACAGTCTTGGGCATCTTTTGGGTTGGAGCACGAGAAATTAGCCATGATGCCTGC
 TTTGCTCAGTCTTTTTTCACTGCTTCTCCTTCCCTCGAGTCCCTCTGTGCTACTGTCTATG
 GCCTTTGACCGCTTTGTGGCTATCTGCCACCCCTTGCACTATGTTTCCATTCTCACCAACAC
 AGTCATTGGCAGGATTGGCCTGGTCTCTCTGGGTCGTAGTGTAGCACTCATTTTTCCATTA
 CCTTTTATGCTCAAAAGATTCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT
 30 CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT
 GTTTGTATCGTCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTTATGCTCTGA
 TCCTGCGCACCGTGCTGTCCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG
 TGTTTCCCACATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTATCC
 ATCGCTTTGGAAAGCAGGCACCCACCTGGTCCAGGTGGTCATGGGTTTCATGTATCTTCT
 35 CTTTCTCCTGTGATGAATCCCATTGTCTACAGTGTGAAGACCAAACAGATCCGGGATCGA
 GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

AOLFR183 sequences:

40 MTNLNASQANHRNFILTGIPGTPDKNPWLAFPLGFLYTLTLLGNGTILAVIKVEPSLHEPTYFYFL
 SILALTDVSLSMSTLPSMLSIYWFNAPQIVFDACIMQMFFIHVFGIVESGLVLSMAFDRFVAIRN
 PLHYVSILTHDVIRKTGISVLTRA VCVFPVPFLIKCLPFCHSNVLSHSYCLHQNMMLRACASTR
 INSLYGLIVVIFTLGLDVLLTLLSYVLTLKTVLGIVSRGERLKTLSLCLSHMSTVLLFYVPFMGA
 ASMIHRFWEHLSPVVMVMADIYLLPVLNPVYSVKTKQI (SEQ ID NO: 337)

45 ATGACGAACCTGAATGCATCACAGGCCAACACCGTAACTTCATTCTGACAGGTATCCCAG
 GAACGCCAGACAAGAACCCTATGGTTGGCCTTTCCCTGGGATTTCTCTACACACTCACACT
 CCTGGGAAATGGTACCATCCTAGCTGTCATCAAGGTGGAGCCAAGTCTCCATGAGCCACG
 TATTACTTCTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC
 ATGCTCAGCATCTACTGGTTTAATGCCCTCAGATTGTTTTTGTGATGCATGCATCATGCAGAT
 50 GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCCTAGTGTCCATGGCCTTTGAC
 AGATTTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCACGATGTTATTG
 AAAGACTGGAATATCTGTCTCACCCGGGCAGTCTGTGTGGTATTCCTGTGCCCTTCCTT
 ATAAAGTGCCTACCTTCTGCCATTCCAATGTCTTGTCTCATTCACTGTCTTCACCAAAA
 CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTCGTC
 55 ATCTTCACACTGGGGCTCGATGTTCTCCTCACTCTACTGTCTTATGTAATCACCTGAAGAC
 TGTGCTGGGCATTGTCTCCAGAGGTGAAAGGCTGAAACCCCTCAGCACATGCCTCTCTCAC

ATGTCTACCGTGCTCCTCTTCTATGTTCTTTTATGGGTGCTGCCTCCATGATCCACAGATT
TTGGGAGCATTTATCACCAGTAGTGACATGGTCATGGCTGATATATACCTACTGCTCCCG
CCTGTGCTAAACCCCATTTGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

- 5 **AOLFR184 sequences:**
MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWWTLPLIAVYLLSALGNGTILWIALQPALHR
PMHFFLFLSVSDIGLVTALMPTLLGIALAGAHTVPASACLLQMVFHVSVMESVLLAMSID
RALAICRPLHYPALLTNGVISKISLAISFRCLGLHLPLPFLAYMPYCLPQVLTHSYCLHPDVARL
ACPEAWGAAYSFLVLSAMGLDPLLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHLSAVLLF
10 YIPMILLALINHPITQHTHTLLSYVHFLPPLINPILYSVKMKEIRKRLNRLQPRKVGAQ
(SEQ ID NO: 339)

- 15 ATGTCAACATTACCAACTCAGATAGCCCCAATAGCAGCACTTCAATGGCCCCACCTTCT
TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCTCCTGGTGGACATTGCCCTCATTGC
TGTCTACCTTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC
GCCCTGCACCGCCAATGCACTTCTTCTCTGCTTAGTGTGTCTGATATTGGATTGGT
CACTGCCCTGATGCCACACTGCTGGGCATCGCCCTTGCTGGTGTCTCACACTGTCCCTGCC
TCAGCCTGCCTTCTACAGATGGTTTTATCCATGTCTTTTCTGTCTGAGTCTCTGTCTT
GCTCGCCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC
20 CTCACCAATGGTGTAAATTAGCAAAATCAGCCTGGCCATTTCTTTTCGATGCCTGGGTCTCC
ATCTGCCCTGCCATTCCTGCTGGCCTACATGCCCTACTGCCTCCACAGGTCTAACCCAT
TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCAGAAGCTTATTTCTTCTCCTAT
ACAGCCTATTTGTGGTTCTTTAGCCATGGGTTTGGACCCCTGCTTATTTCTTCTCCTAT
GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGTGGT
25 CAAACCTGTGCTGCCACCTCTCTGCACTGCTCCTCTTATATCCCTATGATCCTCCTGGC
ACTGATTAACCATCCTGAGCTGCCAATCACTCAGCATAACCCATACTCTTCTATCCTATGTCC
ATTTCTTCTTCTCCTCCATTGATAAACCTATTCTCTATAGTGTCAAGATGAAGGAGATTAGA
AAGAGAATACTCAACAGGTTGCAGCCAGGAAGGTGGGTGGTGTCTCAGTGA (SEQ ID NO:
340)

- 30 **AOLFR185 sequences:**
MFYPILNDISTKNNSNIMSCCNILFIKTVEIILVYNQTSQSPWYPIVPSKSLVYNNNTCFDCYHLQR
VDCVPSRDHINQSMVLASGNSSHPVSVFILLGIPGLESFQLWIAFPFCATYA VAVVGNITLLHVIR
IDHTLHEPMYLF LAMLAITDLVLSSTQPKMLAIFWFHAHEIQYHACLIQVFFHAFSSVESGVL
35 MAMALDCYVATCFPLRHSSILTPSVVIKLGTIVMLRGLLWVSPFCFMVSRMPFCQHQAIPQSYC
EHMAVLKLV CADTSISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA
SHICVILALYIPALFSFLTYRFGHDVPRVVHILFANLYLLIPMLNPIYGVRTKQIGDRVIQCCCG
NIP (SEQ ID NO: 341)

- 40 ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTCTGTT
GTAACATATTATTTATTAACAGTTGAAATTATTCTAGTTTATAATCAAACCCAATCACC
CTGGTATCCAATAGTCCCATCCAAAAGCCTTGATATAATAAACACTTGTGTTGATTGTT
ATCATCTGCAGAGAGTAGATTGCGTTCACAGCAGAGACCATATTAACAGTCCATGGTGCT
GGCTTCAGGGAACAGCTCTTCTCATCCTGTGCTCTCATCCTGCTTGGAAATCCAGGCCTG
45 GAGAGTTTCCAGTTGTGGATTGCCCTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTTGG
AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCTGCATGAGCCCATGTACCTC
TTTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCCTCCTCACTCAACCTAAGATGTT
GGCCATATTCTGGTTTCATGCTCATGAGATTAGTACCATGCCTGCCTCATCCAGGTGTTCT
TCATCCATGCCCTTTTCTTCTGTGGAGTCTGGGGTGTCTATGGCTATGGCCTGGACTGCTAC
50 GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCTGCTTCATGGTGTG
TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCTTCTGCTTCATGGTGTG
CTGAAGTTGGTGTGTGCTGATACAAGCATAAGTCGTGGGTATGGGCTCTTTGTGGCCTTCT
CTGTGGCTGGCTTTGATATGATTGTCATTGGTATGTACATACGTGATGATTTTGAGAGCTGT
55 GCTTCAGTTGCCCTCAGGTGAAGCCCGCTCAAAGCTTTTAGCACACGTGCCTCCCATATC
TGTGTCATCTGGCTCTTTATATCCAGCCCTTTTTCTTCTCCTACCTACCGCTTTGGCCAT

GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT
CAACCCCATCATTTATGGAGTTAGAACAAACAGATCGGGGACAGGGTTATCCAAGGATG
TTGTGGAAACATCCCCTGA (SEQ ID NO: 342)

5 **AOLFR186 sequences:**

MSNASLVTAFLTGLPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
RYTSMMSGSRCALLATGTWLSGSLHSAVQTILTFHLPYCGPNQIQHYFCDAPPILKLACADTSA
NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILRIRTS DGRRRAFQTCASHCIVVLCFFVPCVVIYLR
10 PGSM DAMDGVVAIFYTVLTPLLNPVYTLRNKEVKKAVLKL RDKVAHPQRK (SEQ ID NO:
343)

ATGTCCAACGCCAGCCTCGTGACAGCATTCATCCTCACAGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCTCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
15 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCATGTACTACTTCCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTT
TCCACTTCCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCCTATGATCGCTACTTG
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG
20 CCACCGGCACCTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA
AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTTGTGGACATTGGGATAGT
GGCCTCAGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCTGC
GGATCCGCACCTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT
25 GGTCTTTGCTTCTTTGTTCCCTGTGTTGTCAATTTATCTGAGGCCAGGCTCCATGGATGCCA
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAACTTAGAGACAAAGTAGCACAT
CCTCAGAGGAAATAA (SEQ ID NO: 344)

30 **AOLFR187 sequences:**

MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGPGLLEQLHIWLSIPFCIMYIAALEGNGILI
CVILSQAILHEPMYIFLSMLASADVLLSTTTMPKALANLWLGYSHISFDGCLTQKFFIHFIFIHSA
VLLAMAFDRYVAICSPRYVTILTSKVIGKIVTATLSRSFIIMFPSIFLLEHLHYCQINIIAHTFCEH
MGIAHLSCSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV
35 ILLFYVPALFSVFAYRFGGRSIPCYVHILLASLYVVIPMLNPVIYGVRTKPILEGAKQMFSNLAK
GSK (SEQ ID NO: 345)

ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG
CTATGAACAACTCTGACACTCGCATAGCAGGCTGCTTCCTCACTGGCATCCCTGGGCTGGA
40 GCAACTACATATCTGGCTGTCCATCCCCTTCTGCATCATGTACATCGCTGCCCTGGAAGGC
AATGGCATCCTAATTTGTGTCACTCTCTCCAGGCAATCCTGCATGAGCCCATGTACATAT
TCTTATCTATGCTGGCCAGTGCTGATGTCTTGCTCTCTACCACCACCATGCCTAAGGCCCTG
GCCAATTTGTGGCTAGGTTATAGCCACATTTCTTTGATGGCTGCCTCACTCAAAGTTCTT
CATTCACTTCCTCTTCATTCACTCTGCTGTCTGCTGGCCATGGCCTTTGACCGCTATGTGG
45 CCATCTGCTCCCCCTGCGATATGTCACAATCCTCACAAGCAAGGTCAATGGGAAGATCGT
CACTGCCACCCTGAGCCGCAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC
TGCATATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA
TCTGTCTGTCTGATATCTCCATCAATGTCTGGTATGGGTTGGCAGCTGCTCTTCTCTCCA
CAGGCCTGGACATCATGCTTATTACTGTTTCTACATCCACATCCTCCAAGCAGTCTTCCGC
50 CTCCTTTCTCAAGATGCCCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCATATCTGTGTCA
CCTACTCTTCTATGTCCCTGCCCTTTTTTCTGTCTTTGCCTACAGGTTTGGTGGGAGAAGCA
TCCCATGCTATGTCCATATCTCCTGGCCAGCCTCTACGTTGTCACTTCCTCCTATGCTCAAT
CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTTCA
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

55

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AOLFR188 sequences:

- MFPSLPCPVLLVQLPLMNENMQCFVFCSDSLRMMVSRFIHVFPVKMKRIIVGGYSKHFFSN
 ELLCVRPWSGKTWSIRHHIFDMELLTNNLKFITDPFVCLRLHLSPTPSEEHMKNKNNVTEFILL
 GLTQNPGEQKVLFVTFLLIYMTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK
 5 MIVDLLSEKKTISFQGCMAQLFMDHLFAGAENVLLVMAYDRYMAICKPLHELITMNRVVCVL
 MLLAAWIGGFHLHSLVQFLFIYQLPFCGPNVIDNFLCDLYPLLKACTNTYVTGLSMIANGGAIC
 AVTFTILLSYGVILHSLKTSLEGKRKAFYTCASHVTVVILFFVPCIFLYARPNTSPIDKSMTV
 VLTFTPLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)
- 10 ATGTTCCCCTCCCTGTGTCCATGTGTTCTCCTTGTTCAACTCCCCTTATGAATGAGAACAT
 GCAGTGTGTTTGTGTTTCTGTTCTGTGATAGTTTGCTGAGAATGATGGTTTCCCGCTTCATCC
 ATGTCCCATTTGTAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC
 TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAAAACGTGGTCGATAAGGCATCACAT
 TTTTGACATGGAGCTTCTGACAAATAATCTCAAATTTATCACTGACCTTTTGTGTTGTAGGC
 15 TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAACAATGTGACTG
 AATTTATCCTCTTAGGGCTCACACAGAACCCTGAGGGGCAAAAGGTTTATTTGTACATT
 CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATCATGGCC
 AGCCAGTCCCTGGGTCCCCCATGTACTTTTTCTGGCTCTTTATCATTATAGATACCGT
 CTATTCTACTGCATTTGCTCCAAAATGATTGTTGACTTGCTCTGAGAAAAAGACCATTT
 20 CCTTCAGGGTTGTATGGCTCAACTTTTTATGGATCATTATTTGCTGGTGCTGAAGTCATT
 CTCTGGTGTAATGGCCTATGATCGATACATGGCCATCTGTAAGCCTCTTCATGAATTGA
 TCACCATGAATCGTCGAGTCTGTGTTCTTATGCTGTTGGCGGCTGGATTGGAGGCTTTCT
 TCACTCATTGGTTCAATTTCTCTTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCATTG
 ACAACTTCTGTGTGATTTGTATCCCTTATTGAACTTGCTTGACCAATACCTATGTCAT
 25 GGGCTTTCTATGATAGCTAATGGAGGAGCGATTGTGCTGTACCTTCTTCACTATCCTGC
 TTTCTATGGGTCATATTACACTCTCTTAAGACTCAGAGTTTGAAGGGAAACGAAAGC
 TTTCTACCTGTGCATCCACGTCAGTGTGCTCATTTTATTCTTTGTCCCTGTATCTTCT
 GTATGCAAGGCCCAATTCTACTTTTCCCATGATAAATCCATGACTGTAGTTCTAATTTTA
 TAACTCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT
 30 GAGGAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA
 (SEQ ID NO: 348)

AOLFR189 sequences:

- MQQNSVPEFILLGLTQDPLRQKIVFVIFLYMGTVVGNMLIIVTIKSSRTLGSPPMYFFLYLSF
 35 ADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDYVAICKPLRYP
 TIMSQVQVCHILIVLAWIGSLIHSTAQILALRLPFCGPYLIDHYCCDLQPLLKACMDTYMINLLL
 VNSGAICSSFMILIYSIVILHSLRNHSAKGKKKALSACTSHIIVILFFGPCIFIYTRPPTTFPMD
 KMAVVFYTGTPFLNPLIYTSEECRSEKCHEK (SEQ ID NO: 349)
- 40 ATGCAGCAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCTTGA
 GGCAGAAAATAGTGTGTTGTAATCTTCTTAATTTCTATATGGGAAGTGGTGGGGAATAT
 GCTCATTATTGTGACCATCAAGTCCAGCCGACACTAGGAAGCCCCATGTACTTCTTTCTA
 TTTATTTGTCTTTGCAGATTCTTGCTTTTCAACTCCACAGCCCCATGATTAATTGTGGA
 TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTTGCACTA
 45 CATTTATTTGGCTGCATGGAGATCTTTGCTCTCATTCTCATGGCTGTTGATCGCTATGTGGC
 CATCTGTAAGCCCTTGCGTTACCCAACCATCATGAGCCAGCAGGTCTGCATCATCCTGATT
 GTTCTTGCCCTGGATAGGGTCTTTAATACACTCTACAGCTCAGATTATCCTGGCCTTAAGATT
 GCCTTTCTGTGGACCTATTTGATTGATCATTATTGCTGTGATTGTCAGCCCTTGTGAAAC
 TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG
 50 CTCAAGTAGTTTCATGATTTTGATAATTTTATATATTGTCATCTTGCACTCACTGAGAAACC
 ACAGTGCCAAAGGGAAGAAAAAGGCTCTCTCCGCTTGACGCTCACATAATTGTAGTCAT
 CTTATTCTTTGGCCCATGTATATTATATATACACGCCCCCGACCACTTTCCCATGGACA
 AGATGGTGGCAGTATTTTATACTATTGGAACACCCCTTTCTCAATCCACTCATCTACACATCT
 GAGGAATGCAGAAGTGAAAAATGCCATGAGAAAG (SEQ ID NO: 350)
- 55

AOLFR190 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVVFLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN
LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL
YAQTMPRRLCICLVLYSYTGGFVNAILTSNTFTLDFCGDNVIDDFCDVPPLVKLACSVRESYQ
5 AVLHFLLASNVISPTVLILASYLSIITLRIHSTQGRIKVFSTCSSHLISVTLYYGSILYNYSRPSSS
YSLKRDKMVSTFYTMLFPMLNPMIYSLRSKDMKDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGACTGAGTTCATCCTGCTGGGCTTCACCACAGATCCAG
GGATGCAACTGGGCCTCTTTGTGGTGTTCTGCTGGGTGTGTACTGTCTGACTGTGGTAGGAAG
10 TAGCACCTCATCGTGTTGATCTGTAATGACTCCCGCCTACACACACCCATGTATTTTGTCA
TTGGAAATCTGTCAITTTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAAGATCCTAGTG
ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCAGTTCTTCTCTGC
CAGGCTGGCCTATAGTGAGTGCTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC
ATCTCCAAGCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTTT
15 ATATTCCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTCACATTG
GATTTTTGTGGTGACAATGTCATTGATGACTTTTTCTGTGATGTTCCACCCCTCGTGAAGCT
GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCCTTCTGGCCTCCAATGTC
ATCTCCCCTACTGTGCTCATCCTTGCTCTTACCTCTCCATCATCACCACCATCTGAGGAT
CCACTCTACCCAGGGCCGCATCAAAGTCTTCTCCACATGCTCCTCCCACCTGATCTCCGTTA
20 CCTTATACTATGGCTCCATTCTCTACAATACTCCCGGCCAAGTTCAGCTACTCCCTCAAG
AGGGACAAAATGGTTTCTACCTTTTATACTATGCTGTTCCCATGTTGAATCCCATGATCTA
CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTTCAAGTCAGCATAA
(SEQ ID NO: 352)

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AOLFR191 sequences:

MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVIYITSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS
 FIDVCYISSTVPKMLSNLLQEQQTITFVGCHQYFIFSTMGLSECLMTAMAYDRYAAICNPLLYS
 SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCSNVIRHFFCDMPQLLILSCTDTFFVQV
 5 MTAILTMFFGLASALVIMISYGYIGISIMKITSAGSPKAFNTCASHLTAVSLFYTSGIFVYLRSSS
 GGSSSFDRAFASVFYTVVIPMLNPLIYSLRNKEIKDALRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTTCATCCTGCTGGGATTCTCAGATT
 TTCCCAGGATCATAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC
 10 TGGAACCTCTCCCTCATTGTTTTAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT
 CTTCTCAGTAACCTGTCCTTCAATAGATGTCTGCTATATCAGCTCCACAGTCCCCAAGATGC
 TCTCCAACCTCTTACAGGAACAGAACTATCACITTTGTTGGTGTATTATTCAGTACTTT
 ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT
 ATGCTGCCATTTGTAACCCCTGCTCTATTTCATCCATCATGTACCCACCCTCTGTGTTTGG
 15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATTCCAAATTGGTGCTTTGCT
 TCAACTCCACTTCTGTGGGTCTAATGTATCAGACATTTCTTCTGTGACATGCCCCAAGTGT
 TAATCTTGTCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTT
 TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA
 TGAAGATCACTTCAGCTAAAGGCAGTCCAAAGGCATTCAACACCTGTGCTTCTCATCTAAC
 20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTGAGGTCCAGCTCTGGAGGT
 CTTCAAGCTTTGACAGATTTGCATCTGTTTTCTACACTGTGGTCATTCCCATTGTAATCCC
 TTGATTTACAGTTTGAGGAACAAAGAAATTAAAGATGCCTTAAAGAGGTGCAAAAGAGA
 AAGTGCTGCTGA (SEQ ID NO: 354)

25 **AOLFR192 sequences:**

MENNTEVTEFILVGLTDDPELQIPLFVFLFIYLITLVGNLGMIELLLDSCSLHTPMYFFLSNLSLV
 DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMAVDYRAALCKPLHY
 TTTMTTNVCACLAIGSYICGLNASIHTGNTFRLSFCRSNVVEHFFCDAPLLTLSCSDNYISEM
 VIFFVVGFNDFLSILVILISYLFIFITIMKMRSPGRQKAFSTCASHLTAVSIFYGTGIFMYLRPNSS
 30 HFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVKSFAFKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA
 CTGCAGATCCCACTCTTCATAGTCTTCTTTTCATCTACCTCATCACTCTGGTTGGGAACCT
 GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCCATGTACTTCTTCTCA
 35 GTAACCTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG
 GTTCTCACAGGAGACAAATTCATATTATATAATGCTTGTGCCACACAATCTTCTTCTTTG
 TAGCCTTTATCACTGCAGAAAGTTTCTCCTGGCATCAATGGCCTATGACCGCTATGCAGC
 ATTGTGTAAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCCTGGCC
 ATAGGCTCCTACATCTGTGGTTTCTGAATGCATCCATTCTACTGGGAACACTTTACGGC
 40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTTCTGTGATGCTCCTCCTCTCTTGACT
 CTCTCATGTTTCAGACAACTACATCAGTGAGATGGTTATTTTTTTGTGGTGGGATTCAATG
 ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATATTATCACCATCATGAAG
 ATGCGCTCACCTGAAGGACGCCAGAAGGCCCTTTTCTACTTGTGCTTCCCACCTTACTGCAG
 TTCCATCTTTTATGGGACAGGAATCTTTATGTACTTACGACCTAACTCCAGCCATTTTCATG
 45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG
 TCTACAGCCTGAGGAACAAAGAGGTAAAGAGTGCCTTTAAAAAGACTGTAGGGAAGGCAA
 AGGCCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

AOLFR193 sequences:

50 MENKTEVTQFILLGLTNDSELQVPLFITFPFIYITLVGNLGIHVLIFWDSCLHNPMYFFLSNLSLV
 DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMAVDYRAAVCKPLHY
 TTTMTTVCARLAIGSYLGCFLNASIHTGDTFSLSFCKSNEVHHFFCDIPAVMVLSCSDRHISEL
 VLIYVVSFNIFIALLVILISYTFIFITILKMHSASVYQKPLSTCASHFIAVGIFYGTIIFMYLQPSSSH
 SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVKSFAFKKVVEKAKLSVGWSV (SEQ ID NO:
 55 357)

ATGGAAAATAAGACAGAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA
 CTGCAGGTTCCCCTCTTTATAACGTTCCCCTTCATCTATATTATCACTCTGGTTGGAAACCT
 GGGAAATTATTGTATTGATATTCTGGGATTCTGTCTCCACAATCCCATGTACTTTTTTCTCA
 5 GTAACCTGTCTCTAGTGGACTTTTGCTACTCTTCAGCTGTCACTCCCATCGTCATGGCTGGA
 TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAAATGTATATCTTTGT
 AGCTTTTGCCACTGTGGAAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA
 GTGTGCAAACCCCTACATTACACCACAACCATGACAACAACTGTGTGTGCTCGTCTGGCCA
 TAGGCTCCTACCTCTGTGGTTTCTGAATGCCTCCATCCACACTGGGGACACATTTAGTCTC
 10 TCTTTCTGTAAGTCCAATGAAGTCCATCACTTTTTCTGTGATATTCCAGCAGTCATGGTTCT
 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTTCCTTATTTATGTTGTGAGCTTCAATATCT
 TTATAGCTCTCCTGGTTATCTTGATATCCTACACATTCATTTTTATCACCATCCTAAAGATG
 CACTCAGCTTCAGTATACCAGAAAGCCTTTGTCCACCTGTGCCTCTCATTTTCATTGCAGTCGG
 CATCTTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA
 CAGACAAAATGGCACCTGTGTTCTATACAATGGTCATCCCCATGCTGAACCCTCTGGTCTA
 15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT
 GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

AOLFR194 sequences:

20 MERQNSQSCVVEFILLGFSNYPELQGQLFVAFLVIYLVTLIGNAIIIVIVSLDQSLHVPMYLFLNL
 SVVDLSFSAVIMPEMLVVLSTEKTTISFGGCF AQMYFILLFGGAECFLLGAMAYDRFAAICHPL
 NYQMIMNKGVMKLIIFSWALGFMLGTVQTSWSSFPFCGLNEINHISCETPAVLELACADTFL
 FEIYAFTGTFLIILVPFLLILLSYIRVLFALIKMPSTTGRQKAFSTCAAHLTSVTLFYGTASMTYLQ
 PKSGYSPETKKVMSLSYSLTPLLNLIIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO:
 359)

25 ATGGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC
 CTGAGCTCCAGGGCAGCTCTTTGTGGCTTTCCTGGTTATTTATCTGGTGACCCTGATAGG
 AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCCATGTACCTGT
 TTCTCCTGAACTTATCTGTGGTGGACCTGAGTTTCAGTGCAGTTATTATGCCTGAAATGCT
 30 GGTGGTCTCTCTACTGAAAAAACTACAATTTCTTTTGGGGGCTGTTTTGCACAGATGTAT
 TTCATCCTTCTTTTTGGTGGGGCTGAATGTTTTCTTCTGGGAGCAATGGCTTATGACCGATT
 TGCTGCAATTTGCCATCCTCTCAACTACCAAATGATTATGAATAAAGGAGTTTTTATGAAA
 TTAATTATATTTTCATGGGCCTTAGGTTTTATGTTAGGTACTGTTCAAACATCATGGGTATC
 TAGTTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCAGCAGTGT
 35 TAGAACTTGCATGTGCAGACACGTTTTTGTGAAATCTATGCATTACAGGCACCTTTTTG
 ATTATTTTGGTTCCTTTCTTGTGATACTCTTGTCTTACATTGAGTTCTGTTTGCATCCTG
 AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTCCACCTGTGCCGCTCACCTCACAT
 CTGTGACCCTATTCTATGGCACAGCCAGTATGACTTATTTACAACCCAAATCTGGCTACTC
 ACCGGAACCAAGAAAGTGATGTCTTACTCACTTCTGACACCACTGCTGAATCTG
 40 CTTATCTACAGTTTGCAGAAATAGTGAGATGAAGAGGGCTTTGATGAAATTATGGCGAAGG
 CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

AOLFR195 sequences:

45 MIVQLICTVCF LAVNTFHVRSSFDL KADD MGEINQTLVSEFLLGLSGYPKIEIVYFALILVMY
 LVILIGNGVLIASIFDSHFHTPMYFFLGNLSFLDICYTSSSVPSLTVSLISKRNISFSGCAVQMFF
 GFAMGSTECLLLGMMAFD RYVAICNPLRYPHLSKVAYVLMASVSWLSGGINS AVQTLLAMRL
 PFCGNNIINHFACEILAVLKLACADISLNIITMVISNMAFLVPLMVIFFSYMFILYTILOMNSATG
 RRKAFSTCSAHLTVVIIIFYGTIFFMYAKPKSQDLIGEEKLQALDKLISLFYGVVTPMLNPILYSLR
 NKDVKAAVKYLLNKKPIH (SEQ ID NO: 361)

50 ATGATTGTT CAGTTAATTTGTACTGTTTCTTGGCAGTAAATACATTTTCATGTTAGATC
 TTCTTTTGATTTCTGAAAGCAGATGACATGGGTGAGATTAACCAGACACTGTGTGCAGAA
 TTCTTCTTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATTCT
 55 AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTTCTAATCATAGCCAGCATCTTTGATT
 CTCATTTTACACACCAATGTACTTCTTCTGGGCAACCTCTCTTCTGGATATCTGCTAT
 ACATCCTCCTCTGTTCCCTCAACATTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCT

TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGCAATGGGGTCAACAGAATGTCTGCT
 TCTTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC
 ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGCTGCTGGCTGTCCGGTGAATAA
 ATTCAGCTGTGCAAACATTACTTGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA
 5 TCATTTTCGCATGTGAAATATTAGCTGTCTCAAGCTGGCCTGTGCTGATATATCCCTCAATA
 TTATCACCATGGTGATATCAAATATGGCCTTCTGGTTCTTCCACTGATGGTCATTTTTTTC
 TCCTATATGTTTCATCCTCTACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG
 CATTTTCCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTTACGGTACCATCTTCTTT
 ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATTGCAAGCATTAGAC
 10 AAGCTCATTTCTCTGTTTTATGGGGTAGTGACCCCATGCTGAATCCTATACTCTATAGCTT
 GAGAAATAAGGATGTAAAAGCTGCTGTAAAATATTTGCTGAACAAAAACCAATTCATA
 A (SEQ ID NO: 362)

AOLFR196 sequences:

15 MLESNYTMPTEFLVFGFTDYLPLRVTLFLVFLLVYTLTMVGNILLIILVNINSSLQIPMYFLSNL
 SFLDISCSTAITPKMLANFLASRKSISPYGCALQMFFASFADAECILILAAAMAYDRYAAICNPIL
 YTTLMSSRRVCVCFIVLAYFSGSTSLVHVCLTFRLSFCGSNIVNHFFCDIPILLALSCTDTQINQL
 LLFALCSFIQTSTFVVFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS
 20 YSLDIDKVVAVFYTVVFPMPFNPIIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ
 ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTACAGATTATC
 TACCTCTCAGAGTCACACTGTTCTTGGTATTCTTCTGGTATATACATTAACCTATGGTCGGA
 AATATACTCTTAATAATTCTAGTTAATTAATTCAAGCCTTCAAATCCCATGTATTATTT
 25 TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTTCTACAGCAATCACTCCTAAAATGCTGG
 CAAACTTCTTGGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT
 CTTGCTTCTTTTGGTGTGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGCTATG
 CAGCCATGTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT
 CATTTGTGTGGCATATTTTCACTGGAAGTACAACATCACTGGTCCATGTGTGCCTCACATTC
 30 AGGCTGTCTTTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGATATCCACCTCTCT
 GGCTTTATCATGTACAGACACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCACTTCA
 TCCAGACCAGCACTTTTGTGGTAATATTTTCTTACTTCTGCATCCTCATCACTGTGTTG
 AGCATCAAGTCCTCAGGTGGCAGAAAGCAAAACATTCTCCACTTGTGCTTCCACCTCATAG
 CAGTCACCTTATTCTATGGAGCGCTCCTGTTTATGTACTTACAGCCCACCTAGCTATTCC
 35 CTAGACACTGATAAGGTGGTGGCAGTGTTTTATACTGTTGATTTCCCATGTTTAAATCCAA
 TAATTTATAGTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA
 TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAAGAATAGTCAATATCTAA (SEQ ID NO:
 364)

AOLFR197 sequences:

40 MCYLSQLCLSLGEHTLHMGVMVRHTNESNLGFIILGFSDYPQLQKVLFLILLYLLTILGNTTI
 ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGS
 TECVLLALMSCDRYVAVCRPLHYTVLMHHLCMALASMAWLSGIATTLVQSTLTLLQLPFCGH
 RQVDHFICEVPVLIKACVGTTFNEAELFVASILFLVPSFILVSSGYIAHAVLRIKSATRRQKAF
 45 GTCFSLTLVVTIFYGTHFMYLQPAKSRSDQGFVSLFYTVVTRMLNPLIYTLRIKEVKGALKK
 VLAKALGVNIL (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG
 TGAGACATACCAATGAGAGCAACCTAGCAGGTTTCATCCTTTTAGGGTTTCTGATTATCC
 50 TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTGGGGA
 ATACCACCATCATTTCTGGTTTCTCGTCTGGAACCCAAGCTTCATATGCCGATGTATTTCTTC
 CTTTCTCATCTCTCCTTCTGTACCGCTGCTTACCAGCAGTGTTATTTCCAGCTCCTGGT
 AAACCTGTGGGAACCCATGAAAACATATCGCCTATGGTGGCTGTTGGTTCACTTTACAAC
 TCCCATGCCCTGGGATCCACTGAGTGCCTCTTGGCTCTGATGTCCTGTGACCGCTATGT
 55 GGCTGTCTGCCGTCCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG
 CATCTATGGCATGGCTCAGTGAATAGCCACCACCTGGTACAGTCCACCCTACCCTGCA

GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCCTGTGCTCATC
 AAGCTGGCTTGTGTGGGCACCACGTTTAAACGAGGCTGAGCTTTTGTGGCTAGTATCCTTT
 TCCTTATAGTGCCTGTCTCATTTCATCCTGGTCTCCTCTGGCTACATTGCCACGCAGTGTTG
 5 AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTTCGGGACCTGCTTCTCCACCTGACA
 GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT
 CCAGGGACCAGGGCAAGTTTGTCTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC
 TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA
 GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10 **AOLFR198 sequences:**

MENCTEVTKFILLGLTSVPELQIPLFILFTFIYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL
 VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFVALATVENYLLASMAYDRYAAYCKP
 LHYTTMTASVGACALGSYVCGFLNASFHIGGIFSLSFCKSNLVHHFFCDVPAVMALSCSDKH
 TSEVILVFMSSFNIFVLLVIFISYLFIFITILKMHSAGHQKALSTCASHFTAVSVFYGTVIFIYLO
 15 PSSSHSMDTDKMASVIFYAMIIPMLNPVYSLRNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC
 TACAGATCCCCCTCTTTATCTTGTTACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG
 GGGATGATGTTGCTGATCCTGATGGACTCTTGCTCCACACCCCCATGTACTTTTCTCCTCAG
 20 TAACCTGTCTCTGGTGGACTTTGGTACTCCTCAGCTGTCACTCCCAAGGTCATGGCTGGG
 TTCCTTAGAGGAGACAAGGTCATCTCCTACAATGCATGTGCTGTTTCTTCTTTGT
 AGCCTTGGCCACGGTGGAAAATTACTTGTTGGCCTCAATGGCCTATGACCGCTATGCAGCA
 GTGTGCAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCCTGTCTGGCCC
 TAGGCTCATATGTCTGTGGCTTCCTAAATGCCTCATTCACATTGGGGGCATATTCAGTCTC
 25 TCTTTCTGTAAATCCAATCTGGTACATCACTTTTTCTGTGATGTTCCAGCAGTCATGGCTCT
 GTCTTGCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTTATGTCAAGCTTTAATATCT
 TTTTGTCTCTTAGTTATCTTTATCTCCTACTTGTTTCATATTCATCACCATCTTGAAGATGC
 ATTCAGCTAAGGGACACCAAAAAGCATTGTCCACCTGTGCCTCTCACTTCACTGCAGTCTC
 CGTCTTCTATGGGACAGTAATCTTCTACTTGCAGCCCAGCTCCAGCCACTCCATGGAC
 30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCTGTGGTCT
 ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTTGAGAAGGCAAAAAT
 TTCTATAA (SEQ ID NO: 368)

AOLFR199 sequences:

35 MDTGNKTL PQDFLLGFPGSQTQLQSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS
 NLSFLEIWTAAVPAKALAILLGRSQTISFTSCLLQMYFVFSLGCTEYFLAAMAYDRCLAICY
 LHYGAIMSSLLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHHFCDIAPWIALACTNTQA
 VELVAFVIAVVVILSSCLITFVSYYIISTILRIPSASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR
 TSIKDALDLIKA VHV LNTV VTPVLNPFYTLRNKEVRETLLKKWK GK (SEQ ID NO: 369)

40 ATGGACACAGGCAACAAAACCTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCCTGGTTCTC
 AAACCTTTCAGCTCTCTCTCTTTATGCTTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT
 AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCCATGTACTTCTT
 TCTGAGCAACCTCTCCTTCTGGAGATTTGGTATACCACAGCAGCAGTCCCCAAAGCACTG
 45 GCCATCCTACTGGGGAGAAGTCAGACCATATCATTTACAAGCTGTCTTTTGCAGATGTACT
 TTGTTTTCTCATTAGGCTGCACAGAGTACTTCCTCCTGGCAGCCATGGCTTATGACCGCTGT
 CTTGCCATCTGCTATCCTTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC
 TGGCCCTGGGCTCCTGGGTGTGTGGTTTCGTGGCCATTGCAGTGCCACAGCCCTCATCAG
 TGGCCTGTCTTCTGTGGCCCCCGTGCCATCAACCACTTCTTCTGTGACATTGCACCCTGGA
 50 TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT
 GGTATCCTGAGTTCATGCCTCATCACCTTTGTCTCCTATGTGTACATCATCAGCACCATCC
 TCAGGATCCCCCTCTGCCAGTGGCCGGAGCAAAGCCTTCTCCAGTGCTCCTCGCATCTCAC
 CGTGGTGCTCATTTGGTATGGGTCCACAGTTTTCCTTCACGTCCGCACCTCTATCAAAGAT
 GCCTTGGATCTGATCAAAGCTGTCCACGTCTGAACACTGTGGTGACTCCAGTTTAAACC
 55 CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG
 GAAAATAA (SEQ ID NO: 370)

AOLFR200 sequences:

5 MTRKNYTSLEFVLLGLADTLELQILFLFLVIYTLTVLGNLGMILLIRIDSQ LHTPMYFFLANL
SFVDVCNSTTTPKMLADLLSEKKTISFAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL
YSLMSRTVYLKMAAGAFAGLLNFMVNTSHVSSLSFCDNSVIHHFFCDSPPLFKLSCSDTILKE
SISSILAGVNIVGTLLVILSSYSYVLFISFMSHSGEGRHRAFSTCASHLTAILFYATCIYTYLRPSS
SYSLNQDKVASVFYTVVIPMLNPLIYSLRSKEVKALANVISRKRTSSFL (SEQ ID NO: 371)

10 ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC
TGGAGCTACAGATTATCCTCTTTTGTCTTTTCTTGATTTATACACTTACAGTACTGGGA
AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCCAGCTTACACACCCCATGTATTTCTT
CCTGGCTAACCTGTCTTTGTGGACGTTTGTAACTCACTACCATCACCCCAAAGATGCTG
GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTGCTGGCTGCTTCTACAGATGTACT
TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTAAATGGCCTATGACAGGTA
15 TGCGGCCATATGTCGCGCGCTGCTTTACTCCTTGATCATGTCCAGGACCGTCTACCTAAAA
ATGGCAGCCGGGGCTTTGCTGCAGGGTGTGTAACCTCATGGTCAACACAAGCCATGTCA
GCAGCTTGTCATTCTGTGACTCCAATGTCATCCATCACTTCTTCTGTGACAGTCCCCACTT
TTCAAGCTCTCTTGTCTGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG
TGAATATTGTGGGGACTCTGCTTGTCATCCTCTCCTCTACTCCTACGTTCTCTTCTCCATT
20 TTTTCTATGCATTGGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCTCTCACCTGA
CAGCCATAATTCTGTTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCAGCTAC
TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCATGTTGAATC
CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAGGCTTAGCGAATGTAATTAGCA
GGAAAAGGACCTCTCCTTTCTGTGA (SEQ ID NO: 372)

25

AOLFR201 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTSIPSTLVSFLSERKTISLSCAVQMFLGLAMGTTECVLLGMMAFDYVAICNPLR
YPIIMSKDAYVPMAAGSWIIGAVNSAVQSVFVQLPFCRNNINHFTCEILAVMKLACADISDN
30 EFIMLVATTLFILTPLLLIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIIFYGTILFMYMKPKS
KETLNSDDL DATDKIISMFGVMTMPMMNPLIYSLRNKDVKAEV KHLNRRFFSK (SEQ ID NO:
373)

35 ATGGAATGGGAAAACACACCAATTCTGGTGGAATTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTGGACCCTCACCTTACACCCCTATGTAATCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCCTTATCCCTCCACGCTAG
TGAGCTTCCTTTCAGAAAGAAAGACCAATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCT
CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT
40 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTGTTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTGGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT
TGTTTCATATTGACACCTTTGTTATTAATCATTGTCTCTTACACGTTAATCATTGTGAGCATC
45 TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAGCTTCTCTACCTGTTACGCCATCTGA
CTGTGGTCATAATATTCTATGGGACCATCCTCTTCATGTACATGAAGCCCAAGTCTAAAGA
GACACTTAATTCGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAAACAAGGATGTGAAAGAGGCA
GTAAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

50

AOLFR202 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTSIPSTLVSFLSERKTISLSCAVQMFLSLAMGTTECVLLGVMAFDYVAICNPLR
YPIIMSKDAYVPMAAGSWIIGAVNSAVQTVFVQLPFCRNNINHFTCEILAVMKLACADISGN
55 EFILLVTTTLFLLTPLLLIIVSYTLIILSIFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMYMKPKSQ

ETLNSDDLDATDKLIFIFYRVMTMPMMNPLIYSLRNKDVKEAVKHLRRKNFNK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACACACCATTTCTGGTGGAATTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCCTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCTCT
CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGATGGCCTTTGACCGCTAT
10 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCCTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTGTTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTAGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCCTGCTTGTGACCACAACAT
TGTTCTATTGACACCTTTGTTATTAATTATTGTCTCTTACACGTTAATCATTTTGAGCATC
15 TTCAAAATTAGCTCTTCGGAGGGGAGAAGCAAACTTCTCTACCTGCTCAGCTCGTCTGA
CTGTGGTGATAACATTCTGTGGGACCATCTTCCTCATGTACATGAAGCCCAAGTCTCAAGA
GACACTTAATTCAGATGACTTGGATGCCACTGACAACTTATATTCATATTCTACAGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA
GTAAACACCTACTGAGAAGAAAAAATTTTAAACAAGTAA (SEQ ID NO: 376)

20

AOLFR203 sequences:

MKRQNSQSCVVEFILLGFSNPELQVQLFGVFLVIYVVTLMGNAIITVIISLNQSLHVPMYLFLN
LSVVEVSFSAVITPEMLVVLSTEKTMISFVGCFAQMYFILLFGGTECFLLGAMAYDRFAAICHPL
NYPVIMNRGVFMKL VIFSWISGIMVATVQTTWVFSFPFCGPNEINHLFCETPPVLELVCADTFLF
25 EIYFTGTILIVMPFLLILLSYIRVLFALIKMPSTTGRQKAFSTCASHLTSVTLFYGTANMTYLQ
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKRTLKLRWKVILHTF (SEQ ID NO: 377)

ATGAAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCCTGGGCTTTTCTAACTTTC
CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTCTAGTTATTTATGTGGTGACCCTGATGGG
30 AAATGCCATCATTACAGTCATCATCTCCTTAAACCAGAGCCTCCACGTTCCCATGTACCTGT
TCCTCCTGAACCTATCTGTGGTGGAGGTGAGTTTCAGTGCAGTCATTACGCCTGAAATGCT
GGTGGTGCTCTCTACTGAGAAAATATGATTTCTTTTGTGGGCTGTTTGCACAGATGTAT
TTCATCCTTCTTTTGGTGGGACTGAATGTTTTCTCCTGGGAGCGATGGCTTATGACCGATT
TGCTGCAATTTGCCATCCTCTGAACTACCCAGTGATTATGAACAGAGGGGTTTTATGAAA
35 TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTTGGGTAT
TTAGTTTTCCATTTTGTGGCCCCAATGAAATTAATCATCTCTTCTGTGAGACTCCCCCGGTA
CTAGAGCTTGTGTGTGCAGACACCTTCTTATTTGAAATCTATGCCTTCACAGGCACCATTTT
GATTGTTATGGTTCCTTTCTTGTGATCCTCTTGTCTTACATTCGAGTTCTGTTTGCCATCCT
GAAGATGCCATCAACTACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCTCTCACCTCACA
40 TCTGTGACCCTGTTCTATGGCACAGCCAATATGACTTATTTACAACCCAAATCTGGCTACTC
ACCCGAAACCAAGAACTGATCTCATTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTTGATAAACTATGGCGAAGA
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

45 **AOLFR204 sequences:**

MEKKKNVTEFILIGLTQNPIMEKVTFVFLVLYMITLSGNLLIVVTITTSQALSSPMYFFLTHLSL
IDTVYSSSSAPKLIVDSFQEKKIISFNGCMAQAYAEHIFGATEIILLTVMACDCYVAICKPLNYTT
IMSHSLCILLVAVAWVGGFLHATIQILFTVWLPFCGPNVIGHFMCDLYPLLKLVCIDHTLGLFV
AVNSGFICLLNFLILVVSIVILRSLKNSLEGRCKALSTCISHIIVVLFVPCIFVYLRSVTTLPI
50 DKAVAVFYTMVVPMLNPVYTLRNAEVKSAIRKLWRKKVTSND (SEQ ID NO: 379)

ATGGAGAAGAAAAAGAATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCAT
ATGGAGAAAGTCACGTTTGTAGTATTTTGGTCTTTACATGATAACACTTTCAGGCAACC
TGCTCATTGTGGTTACCATACCACCAGCCAGGCTCTGAGCTCCCCCATGTACTTCTTCTG
55 ACCCACCTTTCTTTGATAGACACAGTTTATTCTTCTTCTTACAGCTCCTAAGTTGATTGTGGA
TTCCTTTCAAGAGAAGAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA

15 AOLFR205 sequences:
MESENRTVIREFILLGLTQSQDIQLLVFVLVLIFYFIILPGNFLIFTIKSDPGLTAPLYFFLGNLAFI
DASYSFTVAPRMLVDFLSAKKIISYRGCTQLFFLHFLGGGEGLLVVMFAFDRIAICRPLHYPT
VMNPRTCYAMMLALWLGGFVHSIIQVVLILRLPFCGPNQLDNFFCDVPQVIKLACTDTFVVEL
LMVFNSGLMTLLCFLGLLASYAVILCRIRGSSEAKNKAMSTCITHIIVIFFMFGPGIFIYTRPFRA
FPADKVVSLFHTVIFPLLPVIYTLRNQEVKASMKKVFNKHIA (SEQ ID NO: 381)

AOLFR206 sequences:
MANRNNVTEFILLGLTENPKMQKIIFVVFSVIYTNAMIGNVLIVVTTITASPSLRSPMYFFLAYLSFI
DACYSVNTPKLITDSLYENKTILFNGCMTQVFGHEFFRGVEVILLTVMAYDHYVAICKPLHYT
TIMKQHVCSSLVGVSWWGGFLHATIQILFICQLPCGPNVIDHFMCDLYTLNLACTNHTLGLF
IAANSFGICLLNCLLLLVS CVVILYSLKTHSLEARHEALSTCVSHITVVILSFICFVYMRPPATL
PIDKAVAVFYTMITSMNLNPLYTLRNAQMKNAIKRLCSRKAISSVK (SEQ ID NO: 383)
GGCTTACAGAGAATCCAAAA

143

AAAGCAGTTGCTGTATTCTACACTATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTTCAAG
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIFDSHLHTPMYFFLCN
LSFLDVCTSSSVPLILASFLAVKKKVSFSGCMVQMFISFAMGATECMILGTMALDRYVAICYP
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAMQLPFCANNVIKHFVCEILAILKLACADI
SINVISM TGSNLIVLVIPLLVISISYIFIVATILRIPSTEGKHKAFSTCSAHLTVVIIFYGTIFFMYAKP
10 ESKASVDSGNEDIIEALISLFYGVMTPLNPLIYSLRNKDVKAAVKNILCRKNFSDGK (SEQ ID
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTTCTGCTGGTAGGGCTTTCTGCCCCACC
CAAAGCTCCAGACAGTTTTCTTCGTTCTAATTTTGTGGATGTACCTGATGATCCTGCTTGGA
15 AATGGAGTCCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCCATGTATTTCTT
CCTCTGTAATCTTTCTTCTCCTCGACGTTTGCTACACAAGTTCTCTGTCCCACTAATTTCTG
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCTTCTCTGGGTGTATGGTGCAAAATGTTTAT
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT
GTGGCCATCTGCTACCCACTGAGATACCCTGTCATCATGAGCAAGGGTGCCTATGTGGCCA
20 TGGCAGCTGGGTCCTGGGTCCTGGGCTTGTTGGACTCAGTAGTGCAGACAGCTTTTGCAAT
GCAGTTACCATTCTGTGCTAATAATGTCATTAAACATTTTGTCTGTGAAATTCTGGCTATCT
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTATGACAGGGTGAATCTGAT
TGTTCTGGTTATTCCATTGTTAGTAATTTCCATCTCTTACATATTTATTGTTGCCACTATTCT
GAGGATTCTTCCACTGAAGGAAAACATAAGGCCTTCTCCACCTGCTCAGCCACCTGACA
25 GTGGTGATTATATTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAAGCCT
CTGTTGATTACAGGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC
AAAAACATACTGTGTAGGAAAAACTTTTCTGATGGAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMYLITLLGNIFLISITILDSHLHTPMYFLSNL
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP
LRYPVIMNRRTCQVIAAGSWMTGCLTAMVEMMSVLP LSLCGNSIINHFTCEILAILKLVCVDTS
LVQLIMLVISVLLL PMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFYGTALSMH
35 LKPSAVDSQEIDKFMALVYAGQTPMLNPIIYSLRNKEVKVALKKLLIRNHFNTAFISILK (SEQ
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTTCTTCTGCGGATTTTTTCACTACCC
CAAAGTTCAGGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC
40 AACATTTTTCTGATCTCCATCACCATTCTAGATTCCCACCTGCACACCCCTATGTACCTCTT
CCTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTCTTCTGCCCTCTCTCCAATGCTGG
CAAACCTTTGTTTCAGGGAGAAACACTATTTCAATCTCAGGGTGCGCCACTCAGATGTACCT
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCCATGATGGCATATGACCGGTAT
GTGGCCATCTGCAACCCCTGAGATACCCTGTCATCATGAATAGGAGAACCTGTGTGCAGA
45 TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAAATGATGTCTGTGCT
GCCACTGTCTCTCTGTGGTAATAGCATCATCAATCATTTCACTTGTGAAATTCTGGCCATCT
TGAAATTGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGTACT
TCTTCTCCCCATGCCAATGCTACTCATTGTATCTCTTATGCATTTATCCTCGCCAGTATCC
TGAGAATCAGCTCAGTGAAGGTGGAAGTAAAGCCTTTTCAACGTGCACAGCCACCTGA
50 TGGTGGTAGTTTTGTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGTATGCCGGACAAACCCCATGTTGAAT
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAAGTGGCCTTGAAAAAATTGCTGATTA
GAAATCATTTTAATACTGCCTTCATTCCATCCTCAAATAA (SEQ ID NO: 388)

AOLFR209 sequences:

MDKINQTFVREFILLGLSGYPKLEIIFALILVMYVVILIGNVLIHASILDSRLHMPMYFFLGNLS
 5 FLDICYTTSSIPSTLVSLISKRNISFSGCAVQMFFGFAMGSTECFLGMMAFDRYVAICNPLRY
 PIIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPF CGNNIINHFLCEILAVLKLACSDISVNIV
 TLAVSNIAFLVPLLVIFFSYMFILYTLIRTN SATGRHKAFTCSAHLTVVIIFYGTIFFMYAKPKS
 QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:
 389)

10 ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC
 CCAAACCTTGAGATCATTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC
 AATGGTGTTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTACTTCTT
 CCTGGGCAACCTCTCTTCTGGGATATCTGCTATACAACCTCCTCCATCCCTCAACACTGG
 TGAGCTTAATCTCAAAGAAAAGAAACATTTCTTCTCTGGATGTGCAGTGCAGATGTTCTT
 15 TGGGTTTGCAATGGGGTCAACAGAATGTTTCTCCTTGGCATGATGGCATTGTATGTCGTTAT
 GTGGCCATCTGTAACCTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC
 TGACTTCTGTATCATGGCTTTCTGGTGAATCAATTCAACTGTGCAACATCACTTGCCAT
 GCGATGGCCTTTCTGTGGGAACAATATTATTAATCATTCTTATGCGAGATCTTAGCTGTCC
 TAAATAGCTTGTCTGATATATCTGTCAATATTGTTACCCTAGCAGTGTCAAATATTGCT
 20 TTCTAGTTCTTCTCTGCTCGTGATTTTTTCTCCTATATGTTTCATCCTCTACACCATCTTG
 CGAACGAACTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG
 TGGTGATCATATTTATGGTACCATCTTCTTTATGTATGCAAAACCTAAGTCCCAGGACCTC
 CTTGGGAAAAGACAACTTGCAAGCTACAGAGGGGCTTGTTCATGTTTTATGGGGTTGTGA
 CCCCCATGTTAAACCCATAATCTATAGCTTGAGAAATAAAGATGTAAAGCTGCTATAAA
 25 ATATTTGCTGAGCAGGAAAGCTATTAACAGTAA (SEQ ID NO: 390)

AOLFR210 sequences:

MMGRRNDTNVADFIL TGLSDSEEVQMALFMLFLLIY LITMLGNVGMILLIRLDLQLHTPMYFFL
 30 THLSFIDLSYSTVTPKTLANLLTSNYISFTGCF AQMFVFLGTAECYLLSSMAYDRYAAICSP
 LHYTVIMPKRLCLALITGPYVIGFMDSFVNVSMSRLHFCD SNIHHFFCDTSPILALSCTDTDN
 TEMLIFILAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTIFYGTMIFTYLPK
 RKSYS LGRDQVAPVFYTTIVPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)

35 ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC
 TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT
 GGGGAATGTGGGGATGCTATTGATAATCCGCTGGACCTCCAGCTTCACACTCCCATGTAT
 TTTTCTTACTACCTGTCAATTATTGACCTCAGTTACTCAACTGTGTCGTCACACCTAAAC
 CTTAGCGAACTTACTGACTTCCAATAATTTCTTCTCACGGGCTGCTTGGCCAGATGTTCT
 GTTTTGTCTTCTTGGGTACTGCTGAATGTTATCTTCTCTCCTCAATGGCCTATGATCGCTAT
 40 GCAGCGATCTGCAGTCTCTACACTACACAGTTATTATGCCAAAAGGCTCTGCCTCGCTC
 TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTCCATGAGC
 AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTCTGTGACACTCCCCAATTTT
 AGCTCTGTCTGCACTGACACAGACAACACTGAAATGCTGATATTCATTATCGCTGGTTCC
 ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCT
 45 GAAAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGGCTCTCTCATCTCTTG
 GGAGTCACCATCTTCTATGGAATATGATTTTACTTAAAGCCAAGAAAGTCTTATT
 CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACTATTGTGATCCCATGCTGAATCC
 ACTCATTTATAGTCTTAGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG
 AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)

50

AOLFR211 sequences:

MMGRRNNTNVADFILMGLTSEEIQMALFMLFLLIY LITMLGNVGMILLIRLDLQLHTPMYFFL
 THLSFIDLSYSTVTPKTLANLLTSNYISFTGCF AQMFFFAFLGTAECYLLSSMAHRYAAICSP
 LHYTVIMSKRLCLALITGPYVIGFIDSFVNVSMSRLHFYDSNVHHFFCDTSPILALSCTDTYNT
 55 EILFIIVGSTLMVSLFTISASYVFILFTILKINSTSGKQKAFSTCVSHLLGVTIFYSTLIFTYLPKPK
 SYS LGRDQVASVFYTTIVPVLNPLIYSLRNKEVKNVIRVMQRRQDSR (SEQ ID NO: 393)

ATGATGGGTAGAAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG
 GGAATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATT
 5 TTTTCCTTACTCACCTGTCAATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAACC
 TTAGCGAACTTACTGACTTCCAACATATTTCCCTTACGGGCTGCTTTGCCAGATGTTCTT
 TTTTGCCTTCTTGGGTACTGCTGAATGTTACCTTCTCCTCAATGGCCCATGATCGCTATG
 CAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT
 CATCACTGGGCCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA
 10 GATTGCATTTCTACGACTCAAACGTAATTCATCACTTTTTCTGTGACACTTCCCCAATTTTA
 GCTCTGTCCTGCACTGATACATAACAACCCGAAATCCTGATATTCATTATTGTTGGTTCCAC
 CCTGATGGTGTCCCTTTTCACAATATCTGCATCCTATGTGTTCAATCTCTTTACCATCCTGA
 AAATTAATTCACCTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTGGG
 AGTCACCATCTTTTATAGCACTCTGATTTTACTTATTTAAACCAAGAAAGTCTTATTCCT
 15 TGGGAAGAGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCGTGTGAATCCACT
 CATTTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCATCAGAGTCATGCAGAGAAG
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

AOLFR212 sequences:

20 MAGNNFTEVTVFILSGFANHPQLVSLFLMFLFIYLFVLGNLGLITLIRMSQLHTPMYFFLSN
 LAFIDIFYSSVTVPKALVNFQSNRRSISFVGCFVQMYFFVGLVCCECFLLGSMAYNRYIAICNPL
 LYSVVMQKVSNNWLGVMPIYVIGFTSSLISVWVISSLAFCDSINHFCDTTALLALSCVDTFGT
 EMVSVFLAGFTLLSSLLIITVTYIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLQPD
 NTSSLTQAQVASVFYTVIPMLNPLIYSLRNKDVKNALLRVIHRKLFP (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTTGCAAATCACC
 CTGAATTACAAGTCAGTCTTTTCTTGATGTTTCTCTTCATTTATCTATTCACTGTTTTGGGA
 AACCTGGGACTGATCACGTTAATCAGAATGGATTCTCAGCTTCACACCCCTATGACTTTT
 30 TCCTGAGCAATTTAGCATTTATTGACATATTTTACTCCTCTACTGTAACACCTAAGGCATTG
 GTGAATTTCCAATCCAATCGGAGATCCATCTCCTTTGTTGGCTGCTTTGTTCAATGTACTT
 TTTTGTGGATTGGTGTGTTGTGAGTGTTTCTTCTGGGATCAATGGCCTACAATCGCTACA
 TAGCAATCTGCAATCCCTTACTGTATTCAAGTAGTCATGTCCCAAAAAGTGTCCAACCTGGCT
 GGGAGTAATGCCATATGTGATAGGCTTCACAAGCTCGCTGATATCTGTCTGGGTGATAAGC
 AGTTTGGCGTTCTGTGATTCCAGCATCAATCATTTTTTTGTGACACCACAGCTCTTTTAGC
 35 ACTCTCCTGTGTAGATACATTCCGGCACAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT
 CTTCTTCTCTCTCCTTATCATCACAGTCACCTTATATCATCATCATCTCAGCCATCCTGAG
 GATCCAGTCAGCAGCAGGCAGGCAGAAGGCCTTCTCCACCTGCGCATCCCACCTCATGGCT
 GTAACATCTTTTATGGGTCTCTGATTTTACCTATTTGCAACCTGATAACACATCATCGCT
 GACCCAGGCGCAGGTGGCATCTGTATTCTATACGATTGTCATTCCCATGCTGAATCCACTC
 40 ATCTACAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA
 CTTTTTCCATGA (SEQ ID NO: 396)

AOLFR213 sequences:

45 MNSLGLKLVSMILSAHVFCYSKFNCFGCTHSIPALGADPPGGMGLGNESSLMDFILLGFSDHPRL
 EAVLFVFLVFFYLLTLVGNFTIIISYLDPPPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLQRPKK
 TITYGGCVAQLYISLALGSTECILLADMALDRYIAVCKPLHYVVMNPRLCQQLASISWLSGLA
 SSLIHATFTLQLPLCGNHRDLHFICEVPALLKLACVDTTVNELVLFVVSFLFVVPALISISYGF
 TQAVLRIKSVEARHKAFSTCSSHLTVVIFYGTHIYVYLQPSDSYAQDQKFIISLFYTMVPTLNP
 IYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

50 ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA
 ATTTAATTGTTTGGATGTACCCATTCCATTCCTGCCTTAGGTGCGGATCCCCCTGGAGGG
 ATGGGATTGGGCAATGAGAGTTCCTAATGGATTTTCATCCTTCTAGGCTTCTCAGACCACC
 CTCGTCTGGAGGCTGTTCTCTTTGTATTTGTCCITTTCTTCTACCTCCTGACCCCTGTGGGA
 55 AACTTCACCATAATCATCATCTCATATCTGGATCCCCCTTTCATACCCCAATGTACTTTTT
 TCTCAGCAACCTCTCTTTACTGGACATCTGCTTCACTACTAGCCTTGCTCCTCAGACCTTAG

WO 01/98526

TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTTGCCAACAGC
 TGGCATCTATCTCCTGGCTCAGTGGTTTGGCTAGTTCCTAATCCATGCAACTTTTACCTTG
 5 CAATTGCCTCTCTGTGGCAACCATAGGCTGGACCATTTTATTTGCGAAGTACCAGCTCTTCT
 CAAGTTGGCTTGTGTGGACCACTGTCAATGAATTGGTGGCTTTTGTGTGTAGTGTCTGT
 TTGTTGTCATTCCACCAGCACTCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG
 AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCACCTTACAG
 TGGTGATTATATTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC
 10 CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCACTTTAAATCCT
 ATCATCTATACTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAACTTCTCTCGGA
 AAATTGTGA (SEQ ID NO: 398)

AOLFR214 sequences:

15 MDKSNSSVVSEFVLLGLCSSQKLQLFYCFSSVLYTVIVLGNLLIILTVTSDTSLHSPMYFLLGN
 LSFVDICQASFATPKMIADFLSAHETISFSGCIAQIFFIHLFTGGEMVLLVSMAYDRYVAICKPLY
 YVVMISRRRTCTVLMISWAVSLVHTLSQLSFTVNLPCGPNVDSFFCDLPRVTKLACLSYIIE
 ILIVVNSGILSLSTFSLVSSYIHLVTWLVKSSAAMAKAFSTLASHIAVVILFFGPCIFYVWPFTIS
 20 PLDKFLAIFYTVFTPVLPNPIIYTLNRDMKAAVRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID
 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTACTGTTGGGACTCTGTAGTTCTC
 AAAAATCCAGCTTTTCTATTTTGTCTTCTCTGTGTGTATACAGTCATTGTGCTGGGA
 AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCCTGCACTCCCTATGTACTTCT
 25 CTTGGGAAACCTTTCCTTTGTTGACATTTGTGAGGCTTCTTTTGTACCCCTAAAATGATTG
 CAGATTTTCTGAGTGCACACGAGACCATATCTTTCAGTGGCTGCATAGCCAAATTTCTTT
 ATTCACCTTTTACTGGAGGGGAGATGGTGTCTACTTGTTCGATGGCCTATGACAGGTATG
 TAGCCATATGCAAACCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT
 GGTAATGATCTCCTGGGCTGTGAGCTTGGTGCACACATTAAGCCAGTTATCATTACTGTG
 30 AACCTGCCTTTTGTGGACCTAATGTAGTAGACAGCTTTTTTGTGATCTTCTCGAGTCAC
 CAAACTTGCCTGCCTGGACTCTTACATCATTGAAATACTAATTGTGGTCAATAGTGGAAT
 CTTTCCCTAAGCACTTCTCTCTTGGTCAGCTCCTACATCATTATTCTTGTACAGTTTG
 GCTCAAGTCTTCAGCTGCAATGGCAAAGGCATTTTCTACGCTGGCTTCCCATATTGCAGTA
 GTAATATTATTCTTTGGACCTTGCATCTTACATCTATGTGTGGCCCTTACCATCTCTCCTT
 35 GGATAAATTTCTTGCCATATTTTACACTGTTTTACCCCGTCTAAACCCCAATTATTATA
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAGGAAAATTGTGAACCATACCTGAGGC
 CAAGGAGAATTTCTGAAATGTCAGTAGTAGTGAAGAACTCCTTTCATTAA (SEQ ID NO:
 400)

AOLFR215 sequences:

40 MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYVTSVLGNVLIIVISFDSLNSPMYFLLSNL
 SFIDICQSNFATPKMLVDFFIERKTISFEGCMAQIFVLHSFVGSEMMLLVAMAYDRFIAICKPLH
 YSTIMNRRLCVIFVSISWAVGVLSVSHLAFTVDLPFCGPNEVDSFFCDLPLVIELACMDTYEM
 EIMTLTNSGLISLSCFLALIISYTHLIGVRCRSSGSSKALSTLTAHITVVILFFGPCIFYWPF SRL
 45 PVDKFLSVFYTVCTPLLNPIIYSLRNEDVKAAMWKLNRHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT
 GGGGACTCAACTTTTCTTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC
 AATGTCTTAATTATTGTCAATTATTCTTTTACTCCCATTTGAACTCTCCTATGTACTTCTTG
 50 CTCAGTAATCTTTCTTTTCAATTGATATCTGTGAGTCTAACTTTGCCACCCCAAGATGCTTGT
 AGACTTTTTTATTGAGCGCAAGACTATCTCCTTTGAGGGTTGCATGGCCAGATATTCGTT
 CTTACAGTTTTTGTGGGAGTGAGATGATGTTGCTTGTAGCTATGGCATATGACAGATTTA
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT
 TGTGTCTATTTCTGGGCGGTGGCGTTCTTCACTTGTGTGAGCCACTTGGCTTTTACAGTGG
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTTGTGACCTTCCCTTGGTGATA
 GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGGCCTG

ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCTACACCATCATTTTGATCGGTGTCCG
 ATGCAGGTCCTCCAGTGGGTCATCTAAGGCTCTTTCTACATTAAGTGGCCACATCACAGTG
 GTCATTCTTTTCTTCGGGCCTTGCAITTTATTTCTATATATGGCCTTTTAGCAGACTTCCTGT
 GGACAAATTTCTTTCTGTGTTCTACACTGTTTGTACTCCCTTGTTGAACCCCATCATCTACT
 5 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAAC
 CCTGGAAAACTAG (SEQ ID NO: 402)

AOLFR216 sequences:

MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNSLIVITVIVDPHLHSPMYFLL
 10 TNLSIIDMSLASFATPKMITDYLTGHKTISFDGCLTQIFFLHLFTGTEILLMAMSFDRYIAICKPL
 HYASVISQPVCVALVVASWIMGVMHMSQVIFALTLFPCGPYEVDSEFFCDLPVVFQLACVDY
 VLGLFMISTSGIHALSCFIVLFNSYVIVLVTVKHSSRGSSKALSTCTAHFIVVFLFFGPCIFIYMW
 PLSSFLTDKILSVFYTIFTPTLNPIYTLRNQEVKIAMRKLKNRFLNFKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGCTGGGGCTCTCTAATTCCT
 GGGAACACAGATGTTTTCTTTATGGTGTTTTATTGCTTTATGTGGCAACAATGGTGGG
 TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCCTATGTATTTCC
 TGCTTACCAATCTTTCAATCATTGATATGTCTCTTGCTTCTTTTCGCCACCCCAAAGATGATT
 ACAGATTACCTAACAGGTCACAAAACCATCTCTTTTGATGGCTGCCTTACCCAGATATTCT
 20 TTCTCCACCTTTTCACTGGAAGTGAAGTCATCTTACTCATGGCCATGTCCTTTGATAGGTAT
 ATTGCAATATGCAAGCCCCTGCACTATGCTTCTGTGCTTAGTCCCCAGGTGTGTGTTGCTCT
 CGTGGTGGCTTCCTGGATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTTGCCCTC
 ACGTTACCATCTGTGGTCCCTATGAGGTAGACAGCTTTTTCTGTGACCTTCCTGTGGTGT
 CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGCCTCTTTATGATCTCAACAAGTGGCATA
 25 ATTGCGTTGCTCTGTTTTATTGTTTTATTTAATTCATATGTTATTGCTGGTACTGTGAA
 GCATCATTCTCCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTTATTGTTG
 TCTTCTTGTCTTTTGGGCCATGCATCTTCTATCATGTGGCCACTAAGCAGCTTTCTCACA
 GACAAGATTCTGTCTGTGTTTTATACCATCTTTACTCCCACTCTGAACCAATAATCTATAC
 TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAACTGAAAAATAGGTTTCTAAATTT
 30 TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

AOLFR217 sequences:

MLESFQKSEQMAWSNQSAVTEFILRGLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH
 SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAISFEGCMTQMFFLHLLGGAIEVLLISMFSF
 35 RYVAICKPLHYLTIMSRRMCVGLVILSWIVGIFHALSQLAFTVNLFPFCGPNEVDSEFFCDLPV
 LACVDYILGVFMISTSGMIALVCFILLVISYTHILVTVRQRSSGGSSKALSTCSAHFTVTVLFFGP
 CTFIYVWPFTNFPIDKVLVSVFYTIYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHTP
 (SEQ ID NO: 405)

40 ATGCTAGAGTCCTTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGCGGTAACC
 GAATTCATACTACGGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTTCCTGTTTTT
 CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTCACCATTCATCA
 GAGCCACACCTTCATTCCCCTACGTACTTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC
 CCTGGCCTCATTTGCCACCCCAAAATGATTGCAGACTTCCTTAGAGAACACAAAGCCATC
 45 TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCTACATCTCTTAGGGGGTGTGAGATTG
 TACTGCTGATCTCCATGTCCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA
 ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATACTTCTGATTGTGCGCATCT
 TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCAATGAAGT
 AGACAGTTTCTTTTGTGACCTCCCTTTGGTGATTAACTTGCTTGTGTGACACATATATTC
 50 TGGGGGTGTTTCATGATCTCAACAGTGGCATGATTGCCCTGGTGTGCTTCATCCTCTTGGT
 GATCTCTTACACTATCATCCTGGTCACCGTTCGGCAGCGTTCCTCTGGTGGATCCTCCAAA
 GCCCTCTCCACGTGCAGTGCCCACTTTACTGTTGTGACCCTTTTCTTTGGCCCATGCACTTT
 CATTTATGTGTGGCCTTTCACAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA
 TATACACTCCCCCTCTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC
 55 CATGAGGAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA
 (SEQ ID NO: 406)

NQIHQIFCDFTPVLSLACTDTFLVVIVDAIHAAEIVASFLVIALSYIRIHVILGMHSAEGHHKAFST
CA AHLAVFLLFFGSVAVMYLRF SATYSVFWDTALAVTFVILAPFFNPIIYSLKNKDMKEAIGRLF
HYQKRAGWAGK (SEQ ID NO: 411).

5 ATGAAGCAATATTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTTGTTTCCCTTTTCT
GTGTTACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTGACTGAGTTCCT
CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCTTTATCCCTTGCTTCTCA
TCTACGGATTTATCCTAACTGGAAACCTAATAATGTTTCATTGTCATCCAGGTGGGCATGGC
10 CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCTCTCCTTCCTGGAGATCTGCTATACCA
CAACCACCATCCCCAAGATGCTGTCCTGCCTAATCAGTGAGCAGAAGAGCATTTCCTGTCCTG
TGGCTGCCTCCTGCAGATGTACTTTTCCACTCACTTGGTATCAGAGAAAGCTGTGTCTG
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA
TGATTCCCAAACCTTTGTATCCAGCTGACAGTTGGATCCTGCTTTTGTGGCTTCCTCCTTG
15 CTTCTGAGATTGCATGGATTTCCACCTTGCTTTCTGTGGCTCCAACCAGATCCACCAGAT
ATTCTGTGATTTACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCTAGTGGTCATT
GTGGATGCCATCCATGCAGCGGAAATTGTAGCCTCCTTCCTGGTCATTGCTCTATCCTACA
TCCGGATTATTATAGTGATTCTGGGAATGCACTCAGCTGAAGGTCATCACAAGGCCTTTTC
CACCTGTGCTGCTCACCTTGCTGTGTTCTTGCTATTTTTTGGCAGTGTGGCTGTCTGATT
20 TGAGATTCTCAGCCACCTACTCAGTGTTTTGGGACACAGCAATTGCTGTCACTTTTGTATC
CTTGCTCCCTTTTCAACCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:
412).

AOLFR221 sequences:

25 MRNLSGGHVEEFVLVGFPTTPPLQLLLFVLFVFFAIYLLTLENALIVFTIWLAPSLHRPMYFFLGH
LSFLELWYINVTIPRLAAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP
LLYPSLMPSSLATRLAAASWGSFFSSMMKLLFISQLSYCGPNIINHFFCDISPLNLTCSDEQA
ELVDLLALVMILLPLLA VVSSYTAIIAILRIPTSRGRHKAFSTCAHLAVVVIYYSSTLFTYAR
30 PRAMYTFNHNKIISVLYTHVPPFNPAIYCLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID
NO: 413).

ATGAGAAATTTGAGTGGAGGCCATGTCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC
CTCCCTCCAGCTGCTCCTCTTTGTCTTTTTTTTGCAATTTACCTTCTGACATTGTTGGAGA
ATGCACTTATTGTCTTCACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATGTACTTTTTT
35 CTTGGCCATCTCTCTTTCTGGAGCTATGGTACATCAATGTCAACCATTCCTCGGCTCTTGGC
AGCCTTTCTTACCCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCCAACTGTACTTC
TTTATTGCCTTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT
GGCCATCTGTGGACCCCTCCTTTACCCTAGTCTCATGCTTCCAGTCTGGCCACTCGCCTTG
TGCTGCTCTTGGGGCAGTGGCTTCTCAGCTCCATGATGAAGCTTCTTTTATTTCCCAA
40 TTGTCTACTGTGGACCCAACATTATCAACCACTTTTCTGTGATATTTCCCACTACTCAA
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCCTTCTGGCCCTGGTGATG
ATTCTACTCCCTCTATTGGCTGTGGTTTCATCATACACTGCCATCATTGCAGCCATCCTGAG
GATCCCTACGTCCAGGGGACGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG
GTTGTTATCTACTACTCCTCCACTCTCTTACCTATGCACGGCCCCGGGCCATGTACACCTT
45 CAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAGGAAGACAGTGATGGGCAGAT
GTCATATCCTAGGGATGTTTCAAGACTGA (SEQ ID NO: 414).

AOLFR222 sequences:

50 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLTNSNVFIHAIRLDSHLHTPMYFLSFL
SFSETCYTLGIIPRMLSGLAGGDQAI SYVGCAAQMFFSASWACTNCFLLAAMGFDRYVAICAPL
HYASHMNP TLCAQLVITSFLTGYLFG LGM TLVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPS
ELRIFILSLLVLLVSFFFITISYAYILAAILRIPSAEGQKKAFTSCASHLTVVIIHYGCASFVYLRPK
55 ASYSLERDQLIAMTYTVVTPLLNPVYSLRTRAIQTALRNAFRGRLLGKG (SEQ ID NO: 415).

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ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTTGTCTTCCTGGGCTTCTCCAGTTCTG
 GGGAGTTGCAGCTCCTTCTCTTTGCCTTGTTCCTCTCTGTATCTAGTCACTCTGACCAGC
 AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCATGTACCTCTT
 CCTTTCCCTCCTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT
 5 CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCAGATGTTCTT
 TTCTGCCTCATGGCCTGTACTAACTGCTTCTTCTGGCTGCCATGGGCTTTGACAGATATG
 TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCTCTGTGCCAGCT
 GGTCATTACTTCTCCTGACTGGATACCTCTTGGACTGGGAATGACACTAGTTATTTTCC
 ACCTCTCATTCTGCAGCTCCCATGAAATCCAGCACTTTTTTGTGACACGCCACCTGTGCTG
 10 AGCCTAGCCTGTGGAGATACAGGCCGAGTGAGCTGAGGATCTTATCCTCAGTCTTTTGG
 TCCTCTTGGTCTCCTTCTTCTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG
 AGGATCCCCTCTGCTGAGGGGCAGAAGAAGGCCTTCTCCACTTGTGCCTCGCACCTTACAG
 TGGTCATTATTCTGCTGAGGGGCTTCTTCTGCTGACCTGAGGCCAAAGCCAGCTACTCT
 CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCTTAATCCCA
 15 TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAG
 ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

AOLFR223 sequences:

20 MEAANESSEGISFVLLGLTTSPPGQQRPLFVLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA
 HLSFADLCFASVTPKMLANLLAHDHSISLAGCLTQMYFFALGVTDSCLLAAMAYDCYVAIR
 HPLPYATRMSRAMCAALVGMAWLVSHVSLYILLMARLSFCASHQVPHFFCDHQPLRLSC
 SDTHHIQLLIFTEGAAVVVTPFLLILASYGAIAAAVLQPSASGRLRAVSTCGSHLAVVSLFYGT
 VIAVYFQATSREAEWGRVATVMYTVVTPMLNPIYSLWNRDVQGAIRALLIGRRISASDS
 (SEQ ID NO: 417).

25 ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTTCGTTTTATTGGGACTGACAACAA
 GTCCTGGACAGCAGCGGCTCTCTTTGTGCTGTTCTTGCTCTTGTATGTGGCCAGCCTCCTG
 GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT
 TCCTGCTGGCCACCTGTCTTTGCTGACCTCTGTTTCGCCTCCGTCAGTGTGCCAAGATG
 30 TTGGCCAACTTGTGGCCCATGACCACTCCATCTCGCTGGCTGGCTGCCTGACCCAAATGT
 ACTTCTTCTTTGCCCTGGGGGTAAGTATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG
 CTACGTGGCCATCCGGCACCCCTCCCCTATGCCACGAGGATGTCCCGGGCCATGTGCCGA
 GCCCTGGTGGGAATGGCATGGCTGGTGTCCACGTCCTCCCTCCTGTATATCCTGTCA
 TGGCTCGCTTGTCTTCTGTGCTTCCACCAAGTGCCCACTTCTTCTGTGACCAAGCCT
 35 CTCTTAAGGCTCTCGTGTCTGTACACCCACCATCCAGCTGCTCATCTTACCCAGGGCG
 CCGCAGTGGTGGTCACTCCCTTCTGTGCTTCCACCAAGTGCCCACTTCTTCTGTGACCAAGCCT
 CGTGTCTCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACCTGTGGCTCCCAC
 CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCATTGCAGTCACTTCCAGGCCACATCCC
 GACGCGAGGCAGAGTGGGGCCGTGTGGCACTGTGATGACACTGTAGTACCCCCATGC
 40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGCACTCCGAGCCCTCT
 CATTGGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).

AOLFR224 sequences:

45 MGSFNSTFEDGFILVGFSDWPQLEPILFVFIFYSLTFLGNTIIHLSWLDRLHTPMYFFLSHL
 LDLCFTTSTVPQLINLCGVDRITIRGGCVAQLFIYALGSTECVLLVMAFDRYAAVCRPLHY
 MAIMHPHLCQTLAIASWGAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT
 EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRKAFGTGSHLLVFLFYGSAIYT
 YLQSIHNYSEREGKFVALFYTIITPILNPLIYTLRNKDVKGALWKVLWRGRDSG (SEQ ID NO:
 419).

50 ATGGGAAGTTTCAACACCAGTTTTGAAGATGGCTTCATTTGGTGGGATTCTCAGATTGGC
 CGCAACTGGAGCCCATCCTGTTGTCTTTATTTTATTTTCTACTCCCTAACTCTCTTTGGC
 AACACCATCATCATCGCTCTCTCCTGGCTAGACCTTCGGCTGCACACACCTATGTACTTCTT
 TCTCTCATCTGTCCCTCCTGGACCTCTGCTTACCACACGACCGTGCCCCAGCTCCTGA
 55 TCAACCTTTGCGGGGTGGACCGCACCATACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT
 CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGATGGCCTTGACCGCTAT

GCTGCTGTCTGTCTGCTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCCT
 GGCTATCGCCTCCTGGGGTGC GG GTTTCGTGAACTCTCTGATCCAGACAGGTCTCGCAATG
 GCCATGCCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGCCTGTATTTCTGAA
 GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCCGAGTCATAGT
 5 CGTGGCTGTTTCCTGCAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG
 AGGGTGAAGTCAACGGCTGGGCGCAGAAAAGGCTTTTGGGACTTGTGGGTCCACCTCCTA
 GTAGTTTTCTTTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC
 TGAGCGTGAGGGAAAATTTGTGCCCCTTTTTTATACTATAATTACCCCCATTCTCAATCCTC
 TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG
 10 GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

AOLFR225 sequences:

MENYNQTSTDFILLGLFPFSIIDLFFFILVIFILMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID
 LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLASMA YDRYIAICFPLHYLIRM
 15 SKRVCVLMITGSWIIGSINACAHTVYVLHIPYCRSRAINHHFCDVPAMVTLACMDTWVYEGTV
 FLSATIFLVFPFIGISCSYGQVLFVAVYHMKSAEGRKKAYLTCSTHLTVVTFYAPFVYTYLRPRS
 LRSPTEDKVLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

ATGGAAAATTACAATCAAACATCAACTGATTTTCATCTTATTGGGGCTGTTTCCACCATCAA
 20 TAATTGACCTTTTCTTCTTCATTCTCATTGTTTTCATTTTCCTGATGGCTCTAATTGGAAACC
 TGTCATGATTCTTCTCATCTTCTTGGACACCCATCTCCACACACCCATGTATTTCTACTG
 AGTCAGCTCTCCCTCATTGACCTAAATTACATCTCCACCATGTTCTTAAGATGGCATCTGA
 TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTGAGAGTTTCTTCTTCT
 TGGCATTAGGAGGTGCAGAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGC
 25 TATTGGCTTTCTCTCCACTATCTCATCCGCATGAGCAAAAAGAGTGTGTGTGCTGATGATA
 ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA
 TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCCAGCAATGGTGACT
 CTGGCCTGCATGGACACCTGGGTCTATGAGGGCACAGTGTTTTTGAGTGCCACCATCTTTC
 TCGTGTTTTCCCTTCATTGGTATTTTCATGTTCTATGGCCAGGTTCTCTTTGCTGTCTACCAC
 30 ATGAAATCTGCAGAAGGGAGGAAGAAAGCCTATTTGACCTGCAGCACCCACCTCACTGTA
 GTAACCTTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCC
 AACAGAGGACAAGGTTCTGGCTGTCTTCTACACCATCCTCACCCCAATGCTCAACCCCATC
 ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC
 TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

35

AOLFR226 sequences:

MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLLAYVLVLTENTLIIMAIRNHSTLHKPMYFFL
 ANMSFLEIWYVTVTIPKMLAGFVGSQDHDGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD
 RYMAICYPLHYPVIVSGRLCVQMAAGSWAGGFGISMVKVFLISGLSYCGPNINHFFCDVSPLL
 40 NLCTDMSTAELTDFILAIFILLGPLSVTGASYVAITGAVMHISAAAGRYKAFSTCASHLTVVIIIF
 YAASIFIYARPKALSAFDTNKLVSVLVAVIVPLLNPIIYCLRNQEVKRALCCTLHLYQHQPDP
 KKASRN (SEQ ID NO: 423).

ATGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT
 45 CCTGCGCCACTACAGGTACTATTGTTTGCCCTTTTGCTGCTGGCCTATGTGTTGGTGCTGAC
 TGAGAACACACTCATCATTATGGCAATTAGGAACCATCTACCCTCCACAAACCCATGTAC
 TTTTTTCTAGCTAATATGTCTTTCTGGAGATCTGGTATGTCACTGTCACTATTCCCAAGAT
 GCTTGCTGGCTTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTTGAGGGATGC
 ATGACACAGCTCTACTTTTTCTTGGCTTGGGCTGCACTGAGTGTGTCCTTCTCGCTGTTAT
 50 GGCCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTGAGTGGCC
 GGCTGTGTGTGAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTTGGCATCTCCATGGTCAA
 AGTTTTTCTTATTTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTTCTGTG
 ATGTCTCTCCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTT
 ATCCTGGCCATTTTTATTCTTCTAGGGCCACTCTCTGTCACTGGGGCCTCCTATGTGGCCAT
 55 TACTGGTGCTGTGATGCACATATCTTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT
 GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCATCTATGCTCGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTAAGTGTATGCTGTCATTGTA
CCATTGCTCAATCCCATCATTTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT
GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA
G (SEQ ID NO: 424).

5

AOLFR227 sequences:

MEPQNTSTVTNFQLLGFQNLLEWQALLFVIFLLIYCLTIIGNVVIITVVSQGLRLHSPMYMFLQH
LSFLEVWYTTSTVPLLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP
LRYPLMHRLCARLVVWSWCTGVSTGFLHSMMSRLDFCGRNQINHHFCDLPLMQLSCSR
10 YITEVTIFILSIAVLCICFFLTLPYVIVSSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMVY
CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF
LY (SEQ ID NO: 425).

15

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTCAGCTGTTAGGATTCCAGAACCTTC
TTGAATGGCAGGCCCTGCTCTTTGTCAATTTCTGCTCATCTACTGCCTGACCATTATAGGG
AATGTTGTTCATCATACCGTGGTGAGCCAGGCCCTGCGACTGCACTCCCCTATGTACATGT
TCCTCCAGCATCTCTCCTTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCCCTTCCTA
GCCAACCTGCTGTCTGGGGCCAAGCCATCTCCTTCTCTGCCTGCATGGCACAGCTCTACT
20 TCTTCGTATTCTCGGCGCCACCGAGTGCTTTCTCCTGGCCTTCATGGCCTATGACCGTTAC
CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGT
GGTGGTGGTCTCATGGTGACAGGGGTGACACAGGCTTTCTGCATTCCATGATGATTTC
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTTCTTCTGCGACCTCCCGCCACTCA
TGCAGCTCTCCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCCTGTCAATTGCC
GTGCTGTGCATTTGTTTTTCTGACACTGGGGCCCTATGTTTTTATTGTGTCTCCATATT
25 GAGAATCCCTTCCACCTCTGGCCGGAGAAAGACCTTTTCCACATGTGGCTCCACCTGGCT
GTTGTCACTCTCTACTACGGGACCATGATCTCCATGTATGTGTGTCCCAGTCCCACCTGTT
GCCTGAAATCAACAAGATCATTTCTGTCTTCTACACTGTGGTACACCACTGCTGAACCA
GTTATCTACAGCTTGAGGAACAAAGACTTCAAGAAGCTGTTAGAAAGGTCATGAGAAGG
AAATGTGGTATTCTATGGAGTACAAGTAAAAGGAAGTTCCTTTATTAG (SEQ ID NO: 426).

30

AOLFR229 sequences:

MFYVNQIPFQLYHISFVYPTELWSRAIIPCMPTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK
IILIHDSRLHTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAE
FFLLGLMSCDRYVAICNPLHYPDLMRSRKICWLIVAAA WLGGSIDGFLLPVTMQFFPCASREIN
35 HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRRKAVAT
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQK
VVGRCVSSGKVTTT (SEQ ID NO: 427).

40

ATGTTTTATGTAAATCAGATACCTTTCCAACCTTATCATATCTCTTTCGTGTACCCTACAGA
GCTATGGAGCAGAGCAATTATCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCA
ACGCCCCGTTTCCCCTGGCTTCTTGGCCCTATTCTCCTGGTCTTGTGACCTCCATAGCCAG
CAACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCATGTAATTC
CTGCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTTGTGCCAAAATGCT
45 GGTGACAGGATGATGAGCCAGAGAGCCATTTCTTCTGCTGGATGCACTGCCCAACACTTC
CTCTACTTGACCTTAGCAGGGGCTGAGTCTTCTCCTAGGACTCATGTCTGTGATCGCTA
CGTAGCCATCTGCAACCCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGCTG
ATTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGTCTACCCCGTCACCA
TGCAGTTCCCCTTCTGTGCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTT
CTGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGTGATTATTA
50 TGATGCTCCTCATCCCTTTCTGTGATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT
TATAGGATGAGCGAGGCAGAGGGAGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG
GTGGTTGTGACCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA
CACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT
CCACTCATTTACAGCCTTAGGAACAAGGATGTACGGGGGCCCTACAGAAGGTTGTTGGG
55 AGGTGTGTGCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

AOLFR230 sequences:

MGMEGLLQNSTNFVLTGLITHPAFPGLLFAIVFSIFVVAITANLVMILLIHMDSR LHTPMYFLLS
 QLSIMDTIYICITVPMKMLQDLLSKDKTISFLGCAVQIFLYLTIGGEFFLLGLMAYDRYVAVCNP
 LRYPLLMNRRVCLFMVVGSWVGGSLDGFMLTPVTMSFPFCRSREINHFFCEIPAVLKLSCDTDS
 5 LYETLMYACCVLMLLIPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVSVFYGAIFY
 TNVLPHSYHTPEKDKVVSIFYTILTPMLNPLIYSLRNKDVAAALRKVLGRCGSSQSIRVATVIR
 KG (SEQ ID NO: 429).

ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCTCACAGGCCTCATCACCC
 10 ATCTGCCTTCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA
 GCCAACCTGGTCATGATTCTGCTCATCCACATGGACTCCCGCCTCCACACACCCATGTACTT
 CTTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCCAAGATGC
 TCCAGGACCTCCTGTCCAAGGACAAGACCATTTCCTTCTCTGGGCTGTGCAGTTCAGATCTT
 CCTCTACCTGACCCTGATTGGAGGGGAATTCTTCTCTGCTGGGTCTCATGGCCTATGACCGC
 15 TATGTGGCTGTGTGCAACCCTCTACGGTACCCTCTCCTCATGAACCGCAGGGTTTGCTTATT
 CATGGTGGTTCGGCTCCTGGGTTGGTGGTTCCTTGGATGGGTTTCATGCTGACTCCTGTCACT
 ATGAGTTTCCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTTCTGTGAGATCCCAGCCGT
 GCTGAAGTTGTCTTGACAGACACGTCACTCTATGAGACCCTGATGTATGCCTGCTGCGTG
 CTGATGCTGCTTATCCCTCTATCTGTCTCTGTCTCTACACGCACATCCTCCTGACTGT
 20 CCACAGGATGAACTCTGCTGAGGGCCGGCGCAAAGCCTTTGCTACGTGTTCTCCACATT
 ATGGTGGTGAGCGTTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCCACTCCTACC
 AACTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTCACCCCCATGCTCAA
 CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG
 GAGATGTGGTTCCTCCCAGAGCATCAGGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID
 25 NO: 430).

AOLFR231 sequences:

MERANHSVVSEFILLGLSKSQNLQILFFLGFSVVFVGIVLGNLLILVTVTFDSLHTPMYFLLSNL
 SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLLGGSEMMLLVAMADRYVAICKP
 30 LHYMTIMSPRVL TGLLLSSYAVGVFHSSQMAFMLTLPFCGPNVIDSFCDLPLVIKLACKDTYI
 LQLLVIADSGLLSLVCFLLLLVSYGVIFSVRYRAASRSSKAFSTLSAHITVTVLFFAPCVFIYVW
 PFSRYSDKILSVFYTIFTPLLNPIHTLRNQE VKAAIKRLCI (SEQ ID NO: 431).

ATGGAAAGAGCAAACCATTCAGTGGTATCGGAATTTATTTTGTGGGACTTTCCAAATCTC
 35 AAAATCTTCAGATTTTATTCTTCTTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA
 AACCTGCTCATCTTGGTGACTGTGACCTTTGATTTCGCTCCTTCACACACCAATGTATTTTCT
 GCTTAGCAACCTCTCCTGCATTGATATGATCCTGGCTTCTTTTGTACCCCTAAGATGATTG
 TAGATTTCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATTTCCAGATGTTCTT
 40 TATGCACCTCCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGTAT
 GTTGCCATATGCAAACCCCTCCATTACATGACCATCATGAGCCACGGGTGCTCACTGGGC
 TACTGTTATCCTCCTATGCAGTTGGATTTGTGCACTCATCTAGTCAAATGGCTTTTCATGTTG
 ACTTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTTCTGTGACCTTCCCCTTGTGAT
 TAAACTTGCTGCAAGGACACCTACATCCTACAGCTCCTGGTCAATTGCTGACAGTGGGCTC
 CTGTCACTGGTCTGCTTCTCCTCTTGTCTCCTATGGAGTCATAATATTCTCAGTTAG
 45 GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTCTCCTACTCTCTCAGCTCACATCACAGTTG
 TGACTCTGTTCTTTGCTCCGTGTGTCTTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA
 GATAAAATCTTTCTGTGTTTTACACAATTTTACACCTCTCTTAAATCCTATTATTTATAC
 ATTAAGAAATCAAGAGGTAAGAGCAGCCATTAAAAAAGACTCTGCATATAA (SEQ ID NO:
 432).

50

AOLFR232 sequences:

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV
 VIFVVFMLALSGNAVLILLIHCD AHLHTPMYFFISQLSLMDMAYISVTPKMLLDQVMGVN KIS
 APEGCMQMFFYVTLAGSEFFLATMAYDRYVAICHPLRYPVLMNHRVCLFLSSGCWFLGSVD
 55 GFTFTPTITMFPFRGSREIHFFCEVPAVLNLSCSDTSLYEIFMYLCCVLMLLIPVVISSYLLILL

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TIHGMNSAEGRKKAFATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDDMMVSVFYTLTPVVPN
LIYSLRNKDVGMALKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTTCGATTTTCATCCTGATGGGAC
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG
GTCGGATTTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTGTGTG
GTCATTTTTGTGGTTTTCTCTGATGGCGTTGTCTGGAAATGCTGCTGATCCTTCTGATACA
CTGTGACGCCCACCTCCACACCCCCATGTACTTTTCATCAGTCAATTGTCTCTCATGGACA
TGGCGTACATTTCTGTCACTGTGCCAAGATGCTCCTGGACCAGGTGATGGGTGTGAATAA
10 GATCTCAGCCCCTGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTTCAGAA
TTTTTCCTTCTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA
CCCTGTCCTCATGAACCATAGGGTGTGTCTTCTCTGTCATCAGGCTGCTGGTTCCTGGGCT
CAGTGGATGGCTTCACATTCACCTCCCATCACCATGACCTTCCCCTTCCGTGGATCCCGGA
GATTCATCATTTCTCTGTGAAGTTCCTGCTGTATTGAATCTCTCCTGCTCAGACACCTCAC
15 TCTATGAGATTTTCATGTACTTGTGCTGTGCTCCTCATGCTCCTCATCCCTGTGGTGATCATT
TCAAGCTCCTATTTACTCATCCTCCTCACCATCCACGGGATGAACTCAGCAGAGGGCCGGA
AAAAGGCCTTTGCCACCTGCTCCTCCACCTGACTGTGGTCACTCCTTCTATGGGGCTGCC
ATCTACACCTACATGCTCCCAGCTCCTACCACCCCCTGAGAAGGACATGATGGTATCTG
TCTTCTATACCATCCTCACTCCAGTGGTGAACCTTTAATCTATAGTCTTAGGAATAAGGAT
20 GTCATGGGGGCTCTGAAGAAAATGTAAACAGTGAACCTGCCTTTCAAAAAGCTATGGAG
TAG (SEQ ID NO: 434).

AOLFR233 sequences:

25 MANITRMANHTGKLDFILMGLFRSKHPALLSVVIFVFLKALSGNAVILLIHCD AHLHSPMY
FFISQLSLMDMAYISVTPKMLLDQVMGVNKVSAPECGMQMFLYTLTAGSEFFLATMAYDR
YVAICHPLRYPVLMNHRVCLFLASGCWFLGSVDGFMLTPITMSFPFCRSWEIHFFCEVPAVTI
LSCSDTSLYETLMLCCVLMMLIPVTIHSYLLILLTVHRMNSAEGRKKAFATCSSHLTVVILFY
GAAVYTYMLPSSYHTPEKDDMMVSVFYTLTPVLNPLIYSLRNKDVGMALKMLTVRFVL
(SEQ ID NO: 435).

30 ATGGCCAACATCACCAGGATGGCCAACCACACTGGAAAGTTGGATTTTCATCCTCATGGGAC
TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCACTTTGTGGTTTTCTGAAG
GCGTTGTCTGGAAATGCTGTCTGATCCTTCTGATACACTGTGACGCCACCTCCACAGCC
CCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG
35 CCAAGATGCTCCTGGACCAGGTGATGGGTGTGAATAAGGTCTCAGCCCCTGAGTGTGGG
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTCCGGAATTTTCTTCTAGCCACCATGGC
CTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTACCCTGTCCTCATGAACCATAGG
GTCTGTCTTTTCTGGCATCGGGCTGCTGGTTCCTGGGCTCAGTGGATGGCTTCATGCTCAC
TCCCATCACCATGAGCTTCCCCTTCTGCAGATCCTGGGAGATTCATCATTTCTTCTGTGAAG
40 TCCCTGCTGTAACGATCCTGTCTGCTCAGACACCTCACTCTATGAGACCTCATGTACCTA
TGCTGTGCTCCTCATGCTCCTCATCCCTGTGACGATCATTCAAGCTCCTATTTACTCATCCT
CCTCACCGTCCACAGGATGAACTCAGCAGAGGGCGGAAAAAGGCCTTTGCCACCTGCTCCCA
CTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCCGTCTACACCTACATGCTCCCA
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCC
45 GGTGCTGAACCCCTTTAATCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA
ATGTTAACTGTGAGATTCTGCTCTTAG (SEQ ID NO: 436).

AOLFR234 sequences:

50 MPNSTTVMEFLLMRFSVDVWTLQILHSASFFMLYLVTLMGNILIVTVTCDSSLHMPMYFFLRN
LSILDACYISVTVPTSCVNSLLDSTTISKAGCVAQVFLVFFVYVELLFTIMAHDRYVAVCQPL
HYPVIVNSRICQMTLASLLSGLVYAGMHTGSTFQLPFCSRNVIHQFFCDIPSLKLSCSDTFSNE
VMIVVSALGVGGGCFIIRSYIHIFSTVLGFPRGADRTKAFSTCIPHILVSVFLSSCSSVYLRPP
AIPAATQDLILSGFYSIMPLFNPIIYSLRNKQKVAIKKIMKRIFYSENV (SEQ ID NO: 437).

55 ATGCCCAATTCAACCACCGTATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC
TACAGATTTTACATTCTGCATCCTTCTTATGTTGATTTGGTAACTCTAATGGGAAACATC

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG
 GAATCTGTCTATCTTGGATGCCTGCTACATTCTGTACAGTCCCTACCTCATGTGTCAATT
 CCCTACTGGACAGCACCACCATTCTAAGGCGGGATGTGTAGCTCAGGTCTTCCTCGTGGT
 TTTTTTGTATATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG
 5 TCTGCCAGCCACTTCACTACCCTGTGATCGTGAACCTCTCGAATCTGCATCCAGATGACACT
 GGCCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG
 CCCTTCTGTGCGGTCCAACGTTATTCATCAATTCTTCTGTGACATCCCCTCTCTGCTGAAGCT
 CTCTTGCTCTGACACCTTCAGCAATGAGGTCATGATTGTTGTCTCTGCTCTGGGGGTAGGT
 GGCGGCTGTTTCATCTTTATCATCAGGTCTTACATTACATCTTTTCGACCGTGCTCGGGTT
 10 TCCAAGAGGAGCAGACAGAACAAAGGCCTTTTCCACCTGCATCCCTCACATCCTGGTGGTG
 TCAGTCTTCCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC
 CCAGGATCTGATCCTTTCTGGTTTTTATCCATAATGCCTCCCCTCTTTAACCCTATTATTTA
 CAGTCTTAGAAAATAAGCAAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA
 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

15

AOLFR235 sequences:

MDGVNDSSLQGFVLMGISDHPQLEMIFFLAILFSYLLTLLGNSTIILLRLEARLHTPMYFFLSNL
 SSLDLAFATSSVPQMLINLWGPCKTISYGGCITQLYVFLWLGATECILLVMAFDYVAVCRPL
 RYTAIMNPQLCWLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL
 20 NQAVLNGVCTFFTAVPLSIIVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVFLFYGSASYGY
 LLPAKNSKQDQGKFISLFYSLVTPMVNPLIYTLRNMEVKGALRRLLGKGREVG (SEQ ID NO:
 439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC
 25 CCCAGCTGGAGATGATCTTTTTTATAGCCATCCTCTTCTCCTATTTGCTGACCCTACTTGGG
 AACTCAACCATCATCTTGCTTTCCCGCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT
 CCTCAGCAACCTCTCCTCCTTGGACCTTGCTTTCGCTACTAGTTCAGTCCCCCAAATGCTGA
 TCAATTTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT
 CTTCCTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGTATGGCATTGACCGCTAC
 30 GTGGCAGTGTGCCGGCCCCCTCCGCTACACCGCCATCATGAACCCCCAGCTCTGCTGGCTGC
 TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACTCT
 GCAGTCCCATTTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTGCGAGGTGCCTGCCAT
 GATCAAACCTGGCCTGTGGCGACACAAGTCTCAACCAGGCTGTGCTCAATGGTGTCTGCACC
 TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCCTACTGCCTCATTGCTCAGGCAGT
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCATCT
 GCTGGTGGTGTTCCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC
 AGCAAACAGGACCAGGGCAAGTTCATTTCCCTGTTCTACTCGTTGGTACACCCATGGTGA
 ATCCCCTCATCTACACGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

40

AOLFR236 sequences:

MTSQERDTAIYSINVSFVAKGMTSRSVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL
 LFLLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHLSDLACLSTVTPKVMAGLLTLDGKVIS
 FEGCAVQLYCFHFLASTEFLYTVMAYDRYLAICQPLHYPVAMNRRMCAEMAGITWAIGATH
 45 AAIHTSLTFRLLYCGPCHIAFFCDIPPVLKLACTDTTINELVMLASIGIVAAGCLILIVISYIFIVA
 AVLRIRTAQGRQRAFPCTAQLTGVLLYYVPPVCIYLQPRSEAGAGAPAVFYTIVTPMLNPFYI
 TLRNKEVKHALQRLLCSSFRETAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCCATTAATGTCAGTTTTGTTGCAAAGG
 50 GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA
 CTGTGGTGAGCCACTTCTTCCTGGAGGGTTTGAGGTACACCGCTAAACATTCTAGCCTCTT
 CTTCCTCCTCTTCCTCCTCATCTACAGCATCACTGTGGCTGGGAATCTCCTCATCCTCCTAA
 CTGTGGGCTCTGACTCTCACCTCAGCTTACCCATGTACCACTTCTGGGGCACCTCTCCTTC
 CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTCATGGCAGGCCTGCTGACTCTGG
 55 ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC
 CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC
 TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTTCCGCCTGCTCTACT
 GTGGGCCCTTGCCACATTGCCTACTTCTTCTGCGACATACCCCCTGTCCTAAAGCTCGCCTGT
 ACAGACACCACCATTAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT
 5 GCCTCATCCTCATCGTTATTTCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA
 GCCCAGGGCCGGCAGCGGGCCTTCTCCCCCTGCACTGCCAGCTCACTGGGGTGCTCCTGT
 ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGGC
 CCCTGCTGTCTTCTACACAATCGTAACTCCAATGCTCAACCCATTCAATTACACTTTGCGGA
 ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTTCCGAGAGTCTACAG
 10 CAGGCAGCCCACCCCATAG (SEQ ID NO: 442).

AOLFR237 sequences:

MDQRNYTRVKEFTFLGITQSRELSQVLFTFLFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLL
 RNLSILDICFSSITAPKVLIDLLSETKTISFSGCVTQMFFHLLGGADVFSLSVMAFDRIYAISKPL
 15 HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLLPLVCGPNVLDTFYCDVPQVLKACTDTFT
 LELLMISNNGLVSWFVFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVTVLHFVPCIYVYA
 RPFTALPTDTAISVTFTVISPLLNPIIYTLRNQEMKLAMRKLKRRLGQSERILIQ (SEQ ID NO:
 443).

20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCCTGGGAATTACTCAGTCCC
 GAGAACTGAGCCAGGTCTTATTTACCTTCCTGTTTTTGGTGTACATGACAACTCTAATGGG
 AAACCTTCCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTTCC
 TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCTCCATCACAGCTCCTAAGGTCTG
 ATAGATCTTCTATCAGAGACAAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT
 25 TCTTCCACCTTCTGGGGGGAGCAGACGTTTTTCTCTCTGTGATGGCGTTTGACCGCTAT
 ATAGCCATCTCCAAGCCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC
 TCATCGTGGGCTTCCTGGGTGGGGGGCTTGCCACTCCATAGCGCAGATTTCTCTATTGCT
 CCCACTCCCTGTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCC
 TCAAACCTTGCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTTCAAATAATGGGTT
 30 AGTCAGTTGGTTTGTATTCTTCTTCTCCTCATATCTTACACGGTCATCTTGATGATGCTGA
 GGCTCACACTGGGGAAGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCCACATCACCG
 TGGTGACCCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCCGCCCTTCACTGCCCTCCCC
 ACAGACACTGCCATCTCTGTACCTTCACTGTCTATCTCCCTTTGCTCAATCCTATAATTTA
 CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAAACTGAAGAGACGGCTAGGAC
 35 AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).

AOLFR238 sequences:

MAPENFTRVTEFILTGVSSPELQIPLFLVFLVLYVLTMAGNLGIITLTSVDSRLQTPMYFFLRHL
 AIINLGNSTVIAPKMLMNLVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRYVAICNP
 40 LLYMVVVSRRCLLLVSLTYLYGFSTAIVVSPCIFSVSYCSSNIINHFCYDIAPLLALSCSDTYPE
 TIVFISAATNLFFSMITVLVSFYFNIVLSILRIRSPEGRKKAFTSCASHMIAVTVFYGTMLFMYLQP
 QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:
 445).

45 ATGGCTCCTGAAAATTTACCAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC
 CAGAGCTCCAGATTCCCTCTTCCTGGTCTTCCTAGTGCTCTATGTGCTGACCATGGCAGG
 GAACCTGGGCATCATCACCTCACCAGTGTTGACTCTCGACTTCAAACCCCATGTACTTTT
 TCCTGAGACATCTAGCTATCATCAATCTTGCAACTCTACTGTCAATTGCCCTAAAATGCTG
 ATGAACTTTTAGTAAAGAAGAAACTACCTCATTCTATGAATGTGCCACCAACTGGGAG
 50 GGTCTTGTCTTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA
 TGTGGCCATTTGTAACCTCTGCTCTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGC
 TGGTGTCCCTCACGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTACCTTGTATATTC
 TCTGTGCTTATTGCTCTTCTAATATAATCAATCATTTTTTACTGTGATATTGCACCTCTGTT
 AGCATTATCTTGCTCTGATACTTACATAACCAGAAACAATAGTCTTTATATCTGCAGCAACA
 55 AATTTGTTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTTGTCCATTCTA
 AGGATACGTTACCAGAAGGAAGGAAAAAGCCTTTTCCACCTGCGCTTCGCATATGATA

GCAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT
 CACTGGATACTGATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCTCTATGCTGAATCC
 CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAT
 CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

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AOLFR239 sequences:

MDPQNYSLVSEFVLHGLCTSRHLQNFFFIFFGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG
 NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMQAIFLHFTGGAEMVLLVSMAYDRYVAIC
 KPLHYMTLMSWQTCIRLVLASWVGVFVHSISQVAFVNLPHYCGPNEVDSFFCDLPLVIKLACM
 10 DTYVLGIIMISDSGLLSLSCFLLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLFFGPCIFV
 YVRPFSRFSVDKLLSVFYTIFTPLLNPIIYTLRNEEMKAAMKKLQNRRTVFQ (SEQ ID NO: 447).

ATGGACCCACAGAACTATTCCTTGGTGTCAGAAATTTGTGTTGCATGGACTCTGCACTTCAC
 GACATCTTCAAAATTTTTCTTTATATTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT
 15 AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACTCCTCCCCTATGTACTT
 CCTGCTGGGGAACCTAGCTTTCTGGACATGTGGCTGGCCTCATTTGCCACTCCCAAGATG
 ATCAGGGATTTCTTAGTGATCAAAACTCATCTCCTTTGGAGGATGTATGGCTCAAATCT
 TCTTCTGCACTTTACTGGTGGGGCTGAGATGGTGCTCCTGGTTTCCATGGCCTATGACAG
 ATATGTGGCCATATGCAAACCTTGCATTACATGACTTTGATGAGTTGGCAGACTTGCATC
 20 AGGCTGGTGCTGGCTTCATGGGTCGTTGGATTTGTGCACTCCATCAGTCAAGTGGCTTTCA
 CTGTAAATTTGCCTTACTGTGGCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG
 GTGATCAAACCTTGCCTGCATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG
 GGTGCTTTCCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT
 ATCAGACAGCGTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA
 25 TGGTAGTGACGCTGTTCTTTGGCCCTTGCATTTTGTATTATGTGCGGCCTTTTCAAGTAGGTTT
 TCTGTGGACAAGCTGCTGTCTGTGTTTTATACCATTTTACTCCACTCCTGAACCCCATAT
 CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT
 GACTTTTCAATGA (SEQ ID NO: 448).

AOLFR240 sequences:

MAGENHTTLPEFLLLGFSDLKALQGFLFWVVLVYLVTLLGNSLIILLTQVSPALHSPMYFFLR
 QLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCQAQMYVFIVLGISECCLLTAMAYDRYVAIC
 QPLRYSTLLSPRACLAMVGSSWLTGIITATTHASLIFSLPFRSHPIIPHFLCDILPVLRLASAGKHR
 SEISVMTATIVFIMIPFSLIVTSYIRILGAILAMASTQSRKVFSTCSSHLLVSLFFGTASITYIRPQ
 35 AGSSVTTDRVLSLFYTVITPMLNPIIYTLRNDVRRALRHLVKRQRPS (SEQ ID NO: 449).

ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA
 AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACCTTGCTGGG
 40 TAACTCCCTGATCATCCTCCTCACACAGGTGAGCCCTGCCCTGCACTCCCCATGTACTTCT
 TCCTGCGCCAACCTCTCAGTGGTGGAGCTCTTCTACACCACTGACATCGTGCCAGGACCCT
 GGCCAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCCAGATG
 TACGTCTTCATTGTCCTGGGCATCTCGGAGTGCTGCCTGCTCACGGCCATGGCCTATGACC
 GATATGTTGCCATCTGCCAGCCCCCTACGCTATTCCACCCTCTTGAGCCCACGGGCCTGCTT
 GGCCATGGTGGGGTCTCCTGGCTCACAGGCATCATCACGGCCACCACCCATGCCTCCCTC
 45 ATCTTCTCTACCTTTTCGAGCCACCCGATCATCCCGCACTTTCTCTGTGACATCCTGCC
 AGTACTGAGGCTGGCAAGTGCTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC
 CATAGTCTTCATTATGATCCCCTTCTCTCTGATTGTCACTTCTACATCCGCATCCTGGGTG
 CCATCCTAGCAATGGCCTCCACCCAGAGCCGCCGAAGGTCTTCTCCACCTGCTCCTCCCA
 TCTGCTCGTGGTCTCTCTCTTTTGAACAGCCAGCATCACCTACATCCGGCCGCAGGCA
 50 GGCTCCTCTGTTACCACAGACCGCGTCTCAGTCTCTTCTACACAGTCATCACACCCATGCT
 CAACCCCATCATCTACACCCTTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT
 GAAGAGGCAGCGCCCCCTCACCTGA (SEQ ID NO: 450).

AOLFR241 sequences:

MPQILIFTYLNMFYFFPLQILAENLTMVTEFLLLGFSSLGEIQLALFVVFLFLYLVLSGNVTIIS
 55 VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLNLLSVARTISFNCCALQMFFFLGFAITNCLL

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAACAIGGFLASLTVVNLVFSLPFCSANKVNH
YFCDISAVILLACTNTDVNEFVIFICGVLVLVVPFLFICVSYLCILRTILKIPSAEGRRKAFSTCAS
HLSVVIVHYGCASFIYLRPTANYVSNKDRLVTVTYITVPLNPMVYSLRNKDVQLAIRKVLG
KKGSLKLYN (SEQ ID NO: 451).

5 ATGCCCCAAATTCTTATATTCACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT
CTTGGCAGAAAACCTCACCATGGTCACCGAATTCCTGTTGCTGGGTTTTTCCAGCCTTGGT
GAAATTCAGCTGGCCCTCTTTGTAGTTTTCTTTTTCTGTATCTAGTCATTCTTAGTGGCAA
10 TGTACCATATCAGTGTATCCACCTGGATAAAAGCCTCCACACACCAATGTACTTCTTCC
TTGGCATTCTCTCAACATCTGAGACCTTCTACACCTTTGTCATTCTACCCAAGATGCTCATC
AATCTACTTTCTGTGGCCAGGACAATCTCCTCAACTGTTGTGCTCTTCAATGTTCTTCTT
CCTTGGTTTTTGCATTACCAACTGCCTGCTATTGGGTGTGATGGGTATGATCGCTATGCTG
CCATTTGTCACCCCTCTGCATTACCCCACTCTTATGAGCTGGCAGGTGTGTGAAAACTGGC
15 AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTTAGTTTTAGCC
TCCCTTTTTGTAGCGCCAACAAAGTCAATCATTACTTCTGTGACATCTCAGCAGTCATTCTT
CTGGCTGTACCAACACAGATGTTAACGAATTTGTGATATTCAATTTGTGGAGTTCTTGTAC
TTGTGGTTCCCTTTCTGTTTATCTGTGTTTCTTATCTCTGCATTCTGAGGACTATCCTGAAG
ATCCCTCAGCTGAGGGCAGACGGAAGCGTTTTCCACCTGCGCCTCTCACCTCAGTGTG
20 TTATTGTTTATTATGGCTGTGCTTCTTCTACCTGAGGCTACAGCAAACTATGTGTCC
AACAAGACAGGCTGGTGACGGTGACATACAGATTGTCACTCCATTACTAAACCCCATG
GTTTATAGCCTCAGAAACAAGGATGTCCAACCTGCTATCAGAAAAGTGTGGGCAAGAAA
GGTTCTCTAAAACTATATAATTGA (SEQ ID NO: 452).

AOLFR242 sequences:

25 MNTTLFHPYSFLLLGIPGLESMHLWVGPFPAVFLTAVLGNITLFIQTDSSLHHPMFYFLAILS
SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMAYDCYVAICDPLCY
TLVLTNKVVSVMALAIPLRPLVFVIFVLFILRLPFCGHQIIPHTYGEHMGRIARLSCASIRVNIY
LCAISILVFDIIAIVISYVQILCAVFLSSHARLKAFSTCGSHVCVMLTFYMPAFFSFMTHRFGR
NIPHFHILLANFYVIPPALNSVIYGVRTKQIRAVLKMFFNK (SEQ ID NO: 453).

30 ATGAATACCACTCTATTTATCCTTACTCTTTCTTCTGGAATTCCTGGGCTGGAAAG
TATGCATCTCTGGGTGGTTTTCTTTCTTTGCTGTGTTCTGACAGCTGTCTTGGGAATA
TCACCATCCTTTTTGTGATTGAGACTGACAGTAGTCTCCATCATCCCATGTTCTACTCTCTG
GCCATTCTGTCTATTGACCCGGGCTGTCTACATCCACCATCCCTAAAATGCTTGGCAC
35 CTTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTTATCC
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC
CATCTGTGACCCTCTTTGCTACACGTTGGTGCTGACAAACAAGGTGGTGTGATGGCA
CTGGCCATCTTTCTGAGACCCTTAGTCTTTGTCATACCCTTTGTTCTATTTATCCTAAGGCT
TCCATTTTGTGGACACCAAATTATTCCTCATACTTATGGTGAGCACATGGGCATTGCCCCG
40 CTGCTCTGTGCCAGCATCAGGGTTAATCATCTATGGCTTATGTGCCATCTCTATCCTGGT
CTTTGACATCATAGCAATTGTCATTTCTATGTACAGATCCTTTGTGCTGTATTTCTACTCT
CTTCACATGATGCACGACTCAAGGCATTCAGCACCTGTGGCTCTCATGTGTGTGTCATGTT
GACTTTCTATATGCCTGCATTTTCTCATTCATGACCCATAGGTTTGGTCGGAATATACCTC
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA
45 ATTTATGGTGTGAGAACCAACAGATTAGAGCACAAGTGCTGAAAATGTTTTCAATAAAT
AA (SEQ ID NO: 454).

AOLFR243 sequences:

50 MEQVNKTVVREFVVLGFSSLARLQQLFVIFLLLYLFTLGTNAINSTIVLDRALHTPMYFFLAIL
SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFFGSSHSFLLAAMGYDRYMAICNPLR
YSVLMGHGVCMGLMAAACACGFTVSLVTSLVFHLPHSSNQLHHFFCDISPVKLASQHSFG
SQLVIFMLGVFALVIPLLLILVSIRIISAILKIPSSVGRYKTFSTCASHLIVTVHYSCASFIYLRPK
TNYTSSQDTLISVSYTILPLFNPIMIYSLRNKEFKSALRRITIGQTFYPLS (SEQ ID NO: 455).

55 ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTCGTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTGTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC

AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT
 CCTTGCCATCCTTTCTTGCTCTGAGATTTGCTATACCTTTGTCATTGTACCCAAGATGCTGG
 TTGACCTGCTGTCCCAGAAGAAGACCATTTCCTTCCCTGGGCTGTGCCATCCAAATGTTTTCC
 TTCCTCTTCTTTGGCTCCTCTCACTCCTTCCCTGCTGGCAGCCATGGGCTATGATCGCTATAT
 5 GGCCATCTGTAACCCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGTGTATGGGACTA
 ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCACCACCTCCCTAGTATTTCA
 TCTGCCCTTCCACTCCTCCAACCAGCTCCATCACTTCTTCTGTGACATCTCCCCTGTCCCTA
 AACTGGCATCTCAGCACTCCGGCTTCAGTCAGCTGGTCATATTCATGCTTGGTGTATTTGC
 CTTGGTCAATCCTCTGCTACTTATCCTAGTCTCCTACATCCGCATCATCTCTGCCATTCTAA
 10 AAATCCCTTCCCTCCGTTGGAAGATAACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTGTG
 GTAATGTTCACTACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC
 AAGCCAAGACACCCTAATATCTGTGTCATACACCATCCTTACCCCATTTGTTCAATCCAATG
 ATTTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAAACT
 TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

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AOLFR244 sequences:

MWQEYYFLNVFFPLLKVCCLTINSHVVILLPWECHLIWKILPYIGTTVGSMEEYNTSSTDFTF
 MGLFNRKETSGLIFAIISIIFFALMANGVMIFLIQTDLRLHTPMYFLLSHLSLIDMMYISTIVPKM
 LVNYLLDQRTISFVGCTAQHFLYLTIVGAEFFLLGLMAYDRYVAICNPLRYPVLMSSRRVCWMI
 20 IAGSWFGGSLDGFLLTPITMSFPFCNSREINHFFCEAPAVLKLACADTALYETVMYVCCVLMML
 IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTVVSIFYGAAMYTYMLPHSYHKPAQ
 DKVLSVFYITLTPMLNPLIYSLRNKDVGTGALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCCACTTTTAAAAGTTTGCTGCCTAAC
 25 AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT
 TACCTTATATCGGCACAACGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT
 CACTTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTGGCATCATCTCT
 ATCATCTTCTTACCAGCACTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT
 TGCGCCTTCATACACCCATGTACTTCTCCTCAGCCACCTTTCCTTAATTGACATGATGTAT
 30 ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCATTTCCTT
 TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCTTCTCTG
 CTGGGCCTCATGGCCTATGACCGCTATGTGGCCATTTGCAACCCTCTGAGATACCCTGTCC
 TCATGAGCCGCGGGCTGTGTTGGATGATTATAGCAGGTTCTGCTGTTTGGGGGCTCTTTGGA
 TGGCTTCCCTCTAACCCCATCACCATGAGCTTTCCCTTCTGCAATTCCCGGGAGATTAAACC
 35 ACTTCTTCTGTGAGGCACAGCAGTCTGAAGTTGGCATGTGCAGACACAGCCCTCTACGA
 GACAGTGATGTATGTGTGCTGTGTTTTGATGCTGCTGATTCTTCTCTGTAGTCTTGTCTT
 CCTATGCCCGAATCTGACTACAGTTCAGTGCATGAGCTCAGTGGAGGGCAGGAAGAAGG
 CATTTGCCACTTGCTCATCCACATGACTGTGGTGTCTTGTCTACGGGGCTGCCATGTAC
 ACCTACATGCTGCCACATTCTTACCACAAGCCAGCCAGGACAAAGTCCTCTCTGTGTTTT
 40 ACACCATTTCTACACCCATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC
 TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCTCAAAGGGTGTGAGGAGGTGT
 CTTTTGA (SEQ ID NO: 458).

AOLFR245 sequences:

MDLKNGLSVTEFILLGFFGRWELQIFFVTFSLIYGATVMGNILMVTVTCRSTLHSPLYFLLGN
 45 LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLLIIMAFDRYVAICKP
 LHYRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMNLPFCGHNVINNIFCDLPLVIKLACIETYTLE
 LFVIADSGLLSFTCFILLVSVYIVILVSVPPKSSHGLSKALSTLSAHIIIVTLFFGPCIFIYVWPFSSL
 ASNKTLAVFYTVITPLNPSIYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

50

ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT
 GGGAACCTCAAATTTTCTTCTTTGTGACATTTTCCCTGATCTACGGTGCTACTGTGATGGGA
 AACATTCTCATTATGGTCACAGTGACATGTAGGTCAACCCCTCATTCTCCCTTGTACTTTCT
 CCTTGGAATCTCTCTTTTTTGGACATGTGTCTCTCCACTGCCACAACACCCAAGATGATCA
 55 TAGATTTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT
 CATGCACTTCTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG
 TTTGCGATACTTTTCATGGATAATTGGTTTTTACACTCCATAAGCCAGATAGTTTAAACAAT
 GAACTTGCCTTTCTGTGGCCACAATGTCATAAACAACATAATTTGTGATCTTCCCCTTGTA
 TCAAGCTTGCTTGCAATTGAAACATACACCCTGGAATTATTTGTCATTGCTGACAGCGGGCT
 5 GCTCTCTTTCACCTGTTTCATCCTCTTGCTTGTCTTACATTGTCATCCTGGTCAGTGTACC
 AAAAAAATCATCACATGGGCTCTCCAAGGCGCTGTCCACATTGTCTGCCACATCATTGTG
 GTCACCTGTCTTTGGACCTGTATTTTATCTATGTTTGGCCATTAGTAGTTTGGCAAG
 CAATAAACTCTTGCCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA
 CCCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTT
 10 CTGCACAGAATTTCTAG (SEQ ID NO: 460).

AOLFR246 sequences:

MSPENQSSVSEFLLGLPIRPEQQA VFFTLFLGMYLTTVLGNLLIMLLIQLDLHPTMYFFLSH
 LALTDISFSSVTVPKMLMDMRTKYKSILYEECISQMYFFIFFDLDLFLITSMAYDRYVAICHPL
 15 HYTVIMREELCVFLVAVSWILSCASSLSHTLLRLSFCANTIPHVFCDLAALLKLSGSDIFLNE
 LVMFTVGVVITLPMFCILVSYGYIGATILRVPSTKGIHKALSTCGSHLSVSVLYYGSIFGQYLF
 PTVSSSIDKDVIVALMYTVVTPMLNPFYSLRNRDMKEALGKLFSRATFFSW (SEQ ID NO:
 461).

20 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC
 CAGAGCAGCAGGCTGTGTTCTTCACCCTGTTCCCTGGGCATGTACCTGACCACGGTGCTGGG
 GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTCACCTTCACACCCCATGTACTTCT
 TCCTCAGCCACTTGGCTCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
 ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTCTCAGATGTATT
 25 TTTTATAATTTTACTGACCTGGACAGCTTCCTTATTACATCAATGGCATATGACCGATAT
 GTTGCCATATGTACCCCTCTCCACTACACTGTATCATGAGGGAAGAGCTCTGTGCTTCTT
 AGTGGCTGTATCTTGGATTCTGTCTTGTGCCAGCTCCCTCTCTCACACCCTTCTCCTGACCC
 GGCTGTCTTTCTGTGCTGCGAACACCATCCCCATGTCTTCTGTGACCTTGTGCCCCTGCTC
 AAGCTGTCTGCTCAGATATCTTCTCAATGAGCTGGTCATGTTACAGTAGGGGTGGTGG
 30 TCATTACCCTGCCATTCATGTGTATCCTGGTATCATATGGCTACATTGGGGCCACCATCCTG
 AGGGTCCCTTCAACCAAAGGGATCCACAAAGCATTGTCCACATGTGGCTCCCATCTCTCTG
 TGGTGTCTCTTATTATGGGTCAATATTTGGCCAGTACCTTTTCCCGACTGTAAGCAGTTCT
 ATTGACAAGGATGTGATTGTGGCTCTCATGTACACGGTGGTCACACCCATGTTGAACCCCT
 TTATCTACAGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAACTCTTCAGTAGAG
 35 CAACATTTTCTCCTTGGTGACATCTGACTTTTTTAAAAAATTAG (SEQ ID NO: 462).

AOLFR247 sequences:

MGQHNLTVLTEFILMELTRRPELQIPFGVFLVIYLLITVVGNLTMILTKLDSHLHPTMYFSIRHL
 ASVDLGNSTVICPKVLANFVDRNTISYYACAAQLAFFLMFIIEFFILSAMAYDRYVAICNPLL
 40 YYVIMSQRQLCHVLVGIQYLYSTFQALMFTIKIFLTFCGSNVISHFYCDDVPLLPMLCSNAQEB
 LLSILFSVFNLISSFLIVLSYMLILLAICQMHSAGEGRKKAFSTCGSHLTVVVVFYGSLLFMYMQ
 PNSTHFFDTDKMASVFYTLVIPMLNPLIYSLRNEEVKNAFYKLFEN (SEQ ID NO: 463).

45 ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAACCTACAAGGCGGC
 CTGAGCTGCAGATTTCCCTTTTTGGAGTCTTCTCGTCATCTACCTAATCACAGTGGTGGGC
 AACCTAACTATGATCATTTTGACCAAAGTGGACTCCCACTACATACACCTATGTACTTTT
 TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTCTACTGTCAATTGTCCCAAGGTGCTGG
 CAAATTTTGTGTGGATCGAAATACTATTTCTATTATGCATGTGCTGCACAGCTGGCATTG
 50 TTCCTTATGTTTATTATCAGTGAATTTTTCATCCTGTGAGCCATGGCCTATGACCGCTATGT
 GGCCATTTGTAACCCCTCTGCTCTATTATGTTATTATGTCTCAGCGACTGTGTCATGTACTGG
 TTGACCTTCTGTGGCTCTAATGTCATCAGTCATTTTACTGTGATGATGTTCTTTGCTACC
 TATGCTTTGCTCAAATGCACAGGAAATAGAATTGTTGAGCATACTATTTCTGTATTTAATT
 TGATCTCCTCCTTTCTGATAGTCTTAGTGTCTACATGTTGATTTTGTAGCTATATGTCAA
 55 ATGCATTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTTCCTTTGACAGTGG
 TGGTGTGTTCTATGGGTCTTACTCTTCATGTACATGCAGCCCAATCCCACTCACTTCTT

GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCCTTTGAT
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAAATTGA
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPALPTGGLLPHQHTMMEIANVSSPEVFVLLGFSTRPSLETVLFIVVLSFYMVLSILNGI
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWL
ATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTSMVGSTLTMLPLCG
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVPLPLGLILVSYGHIARAVLKIRSAEGR
10 RKAFTNCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGKFIALFYTVVTPALNPLIYTLRNTEVKS
ALRHMVLENC CGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT
GATGGAAATAGCCAATGTGAGTTCTCCAGAAGTCTTTGTCCTCCTGGGCTTCTCCACACGA
15 CCCTCACTAGAACTGTCCTCTTCATAGTTGTCTTGAGTTTTTACATGGTATCGATCTTGGG
CAATGGCATCATCATTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT
TTCTTGCCAACTCCCTTCTGGACATGAGCTTACCACGAGCATTGTCCACAGCTCCTG
GCTAACCTCTGGGGACCACAGAAAACCATAAGCTATGGAGGGTGTGTGGTCCAGTTCTAT
ATCTCCCATTTGGCTGGGGGCAACCGAGTGTGTCCTGCTGGCCACCATGTCCTATGACCGCT
20 ACGCTGCCATCTGCAGGCCACTCCATTACACTGTCATTATGCATCCACAGCTTTGCCTTGG
GCTAGCTTTGGCCTCCTGGCTGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTGCGAGATGCCCCCTCA
TTATGCAACTGGCTTGTGTGGATACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCTT
TGTCTTTGTTGTCCTGCCTCTGGGGCTCATCCTGGTCTCTTACGGCCACATTGCCCGGGCCG
25 TGTTGAAGATCAGGTCAGCAGAAGGGCGGAGAAAGGCATTCAACACCTGTTCTTCCCACG
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAGAG
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG
AACCCACTTATTTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

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AOLFR249 sequences:

MKSQIEKSDLKYRAILLQKVTRMFLFWVLLLVLRLVVMGRGNSTEVTEFHLLGFGVQHEF
QHVLFIVLLLIYVTSIGNIGMILLIKTDSRLQTPMYFFPQHLLAFVDICYTSAITPKMLQSFTEN
NLITFRGCVIQLVYATFATSDCYLLAMAMDCYVAICKPLRYPMIMSQT VYIQLVAGSYIIGSI
35 NASVHTGFTFSLFCKSNKINHFFCDGLPILALSCSNIDINILDVVFVGFDFLMFTELVIIFSYYIM
VTILKMSSTAGRKKSFSSTCASHLTA VTIFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAAGTGACTTAAAATATAGAGCCATTTTATTGCAAAAAGTC
40 ACAAGGATGTTCTGCTTTTCTGGGTCCTTCTCTTGGTCCTTTCTAGACTTTTGGTAGTCAT
GGGTCGAGGAAACAGCACTGAAGTGACTGAATTCCATCTTCTGGGATTTGGTGTCCAACAC
GAATTTAGCATGTCTTTTCACTGACTTCTTCTTATCTATGTGACCTCCCTGATAGGAAA
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTTCAAACACCCATGTACTTTTTTC
45 CACAACATTTGGCTTTTGTGATATCTGTTATACTTCTGCTATCACTCCCAAGATGCTCCAA
AGCTTCACAGAAGAAAATAATTTGATAACATTTGGGGGCTGTGTGATACAATTCTTAGTTT
ATGCAACATTTGCAACCAGTGACTGTTACCTCCTAGCTATTATGGCAATGGATTGTTATGT
TGCCATCTGTAAGCCCCCTTCGCTATCCCATGATCATGTCCCAAACAGTCTACATCCAACCTCG
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTACATTTTCA
CTGTCCTTCTGCAAGTCTAATAAAATCAATCACTTTTTCTGTGATGGTCTCCCAATTCTTGC
50 CCTTTCATGCTCCAACATTGACATCAACATCATTCTAGATGTTGTCTTTGTGGGATTTGACT
TGATGTTCACTGAGTTGGTCATCATCTTTCTTACATCTACATTATGGTCACCATCCTGAAG
ATGCTTCTACTGCTGGGAGGAAAAAATCCTTCTCCACATGTGCCTCCCACCTGACAGCAG
TAACCAATTTCTATGGGACACTCTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG
GAGAATATGAAAGTAGCCTCTATATTTATGGCACTGTTATCCCATGTTGAATCCTTTAAT
55 CTATAGCTTGAGAAATAAGGAAGGAAATAA (SEQ ID NO: 468).

AOLFR250 sequences:

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIILAIGSDLHLHTPMYFFLANLSFV
 DMGLTSSVTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLSFFLAAMAYDRYVAICHPLCY
 STVMRPQVCALMLALCWVLTNIVALHTHFLMARLSFCVTGEIAHFFCDITPVLKLSGSDTHINE
 5 MMVFLVGGTVLIVPFLCIVTSYIHVPAILRVTRGGVGKAFSTCSSHLCVVCVFGTLFSAYLC
 PPSIASEEKDIAAAAMYTIVTPMLNPFYSLRNKDMKGALKRFLSHRSIVSS (SEQ ID NO: 469).

ATGGAAAACCAATCCAGCATTTCTGAATTTTCTCCGAGGAATATCAGCGCCTCCAGAGC
 AACAGCAGTCCCTCTTCGGAATTTTCTGTGTATGTATCTTGTACCTTGACTGGGAACCTG
 10 CTCATCATCTGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTCTTGGC
 CAACCTGTCTTTTGTGACATGGGTTTAAACGTCCTCCACAGTTACCAAGATGCTGGTGAAT
 ATACAGACTCGGCATCACACCATCTCCTATACGGGTTGCCTCACGCAAATGTATTTCTTTCT
 GATGTTTGGTGATCTAGACAGCTTCTCCTGGCTGCCATGGCGTATGACCGCTATGTGGCC
 ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC
 15 ATTGCTGTGGGTCTCACCATAATCGTTGCCCTGACTCACACGTTCTCATGGCTCGGTTGT
 CCTTCTGTGTGACTGGGGAAATTGCTCACTTTTCTGTGACATCACTCCTGTCTGAAGCTG
 TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTTGTCTTGGGAGGCACCGTACTCA
 TCGTCCCCTTTTATGCATTGTACCTCCTACATCCACATTGTGCCAGCTATCCTGAGGGTC
 CGAACCCGTGGTGGGGTGGGCAAGGCCTTTTCCACCTGCAGTCCCACTCTGCGTTGTTT
 20 GTGTGTTCTATGGGACCCTCTTCAGTGCCTACCTGTGTCTCCCTCCATTGCCTCTGAAGAG
 AAGGACATTGCAGCAGCTGCAATGTACACCATAGTGAAGTCCCATGTTGAACCCCTTTATCT
 ATAGCCTAAGGAACAAGGACATGAAGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA
 TTGTTTCTCTTAG (SEQ ID NO: 470).

AOLFR251 sequences:

MEGNKTWITDITLPRFQVGPALAILLCGLFSAFYTLTLLGNVIFGHIICLDCKLHTPMYFFLSHLA
 IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFHVECLILVMSYDRYADICHPLRY
 NILMSWRVCTVLAVASWVFSLLALVPLVLILRPLFCGPHEINHFCILSVLKLACADTWLNQV
 VIFAACVFILVGPLCLVLVSYLRLAILRIQSGEGRRKAFSTCSSHLCVVGFFGSAIVTYMAPK
 30 SRHPEEQQKVLVSLFYSLFNPLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA
 GCACTGGAGATTCTCCTCTGTGGACTTTTCTCTGCCTTCTATACACTCACCTGCTGGGGAA
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCCATGTACTTCTTCC
 35 TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCAATATGTCCCAAGATGCTGACG
 AATCTTATGAACCAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAGACATTCTTGT
 ATTTGGCTTTTGTCTACGTAGAGTGTCTGATTTTGGTGGTGATGTCCTATGATCGCTATGCG
 GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGCACTGTCTGCG
 CTGTGGCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT
 40 CTGCCCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT
 GGCCTGTGCTGACACCTGGCTCAACCAGGTGGTCATCTTTCAGCCTGCGTGTTCATCCTG
 GTGGGGCCACTCTGCCTGGTGTGCTGCTCCTACTTGCATCCTGGCCGCGCATCTTGAGGA
 TCCAGTCTGGGGAGGGCCGAGAAAGGCCTTCTCCACCTGCTCCTCCACCTTTGCGTGCT
 GGGACTCTTCTTTGGCAGCGCCATTGTACGTACATGGCCCCCAAGTCCCGCCATCCTGAG
 45 GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA
 TATATAGCCTAAGGAATGCAGAGGTCAAGGGCGCCCTGAGGAGGGCACTGAGGAAGGAG
 AGGCTGACGTGA (SEQ ID NO: 472).

AOLFR252 sequences:

MRLANQTLGGDFLLGIFSQISHPGRLCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL
 50 IDLTYSIVTPKMLVNQLAKDKTISVLGCGTQMYFYQLGGAECCLLAAMAYDRYVAICHPLR
 YSVLMSHRVCLLLASGCWFVGSVDGFMPLPIAMSFPFCSHEIQHFFCEVPAVLKLSGSDTSLY
 KIFMYLCCVIMLLIPVTVISVSYYYIILTIHKMNSVEGRKKAFTTCSHITVVSIFYGAAIYNYML
 PSSYQTPEKDMSSFFYTILTPVLNPIIYSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

ATGCGGCTGGCCAACCAGACCCTGGGTGGTGACTTTTTCTCTGTTGGGAATCTTCAGCCAGA
 TCTCACACCCTGGCCGCCTCTGCTTGCTTATCTTCAGTATATTTTTGATGGCTGTGTCTTGG
 AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACTCCCATGTACTTCTT
 TATAAACCAGCTCTCACTCATAGACTTGACATATAATTTCTGTCACTGTCCCCAAAATGCTG
 5 GTGAACCAGCTGGCCAAAGACAAGACCATCTCGGTCCTTGGGTGTGGCACCCAGATGTAC
 TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT
 ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC
 CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA
 TGAGCTTCCCCTTCTGCAGATCCCATGAGATTGAGCACTTCTTCTGTGAGGTCCCTGCTGTT
 10 TTGAAGCTCTCTTGCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT
 CATGCTCCTGATACCTGTGACGGTCATTTCAAGTGTCTTACTACTATATCATCTCACCATCC
 ATAAGATGAACTCAGTTGAGGGTCGGAAAAAGGCCTTCACCACCTGCTCCTCCCACATTAC
 AGTGGTCAGCCTCTTCTATGGAGCTGCTATTTACAACCTACATGCTCCCCAGCTCCTACCAA
 ACTCCTGAGAAAGATATGATGTCATCCTTTTTCTACACTATCCTTACACCTGTCTTGAATCC
 15 TATCATTTACAGTTTCAGGAATAAGGATGTCACAAGGGCTTGAaaaaaATGCTGAGCGT
 GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

AOLFR253 sequences:

MTFFSSGGNCEPVMCSGNQTSQNQTASTDFTLTGLFAESKHAALLYTVTFLLFLMALTGNALL
 20 ILLIHSEPRLHTPMYFFISQLALMDLMYLCVTPKMLVGQVTGDDTISPSGCGIQMFFHLTLAG
 AEVFLLAAMAYDRYAAVCRPLHYPLLMNQRCQLLVSACWVLGMVDGLLLTPITMSFPFCQS
 RKILSFFCETPALLKLSCSDVSLYKMLTYLCCILMLLTPIMVISSSYTLILHLIHRMNSAAGRKA
 LATCSSHMIIIVLLFGASFYTYMLRSSYHTAEQDMMVSAFYTIFTPVLNPLIYSLRNKDVTRAL
 RSMMQSRMNQEK (SEQ ID NO: 475).

ATGACTTTTTTTCTCTCAGGGGGAAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT
 CTCAGAATCAAACAGCAAGCACTGATTTACCCCTCACGGGACTCTTTGCTGAGAGCAAGCA
 TGCTGCCCTCCTCTACACCGTGACCTTCCTTCTTTCTTGATGGCCCTCACTGGGAATGCCC
 30 TCCTCATCCTCCTCATCCACTCAGAGCCCCGCCTCCACACCCCCATGTACTTCTTCATCAGC
 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCCAAGATGCTTGTGGGCC
 AGGTCACTGGAGATGATACCATTTCCCCGTCAGGCTGTGGGATCCAGATGTTCTTCCACCT
 GACCCTGGCTGGAGCTGAGGTTTTCTCTCCTGGCTGCCATGGCCTATGACCGATATGCTGCT
 GTTTCAGACCTCTCCATTACCCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT
 CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTGCTCACCCCCATTACCATGAGCTT
 35 CCCCTTTTGCCAGTCTAGGAAAATCCTGAGTTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC
 TCTCCTGCTCTGACGTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT
 CTCACCCCCATCATGGTCATCTCCAGCTCATACACCTCATCCTGCATCTCATCCACAGGAT
 GAATTCTGCCGCCGGCCGAGGAAGGCCTTGGCCACCTGCTCCTCCCACATGATCATAGTG
 CTGCTGCTCTTCGGTGCTTCTTCTACACCTACATGCTCCGGAGTTCTTACCACACAGCTGA
 40 GCAGGACATGATGGTGTCTGCCTTTTACACCATCTTCACTCCTGTGCTGAACCCCTCATTT
 ACAGTCTCCGCAACAAAGATGTCACCAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA
 ACCAAGAAAAGTAG (SEQ ID NO: 476).

AOLFR254 sequences:

MTNTSSDFTLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI
 45 MDTLFICTTVPKLLADMVSKEKHSFVACGIQIFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP
 VLMNRKKCLLLAAGAWFGGSLDGFLLPITMNPVPCGSR SINHFFCEIPAVLKLACADTSLYET
 LMYICCVLMILLIPISIISTSYSLILLTIHRMPSAEGRKKAFTTCSHLTVVSIFYGAAFYTYVLPQS
 FHTPEQDKVVSAFYTIVTPMLNPLIYSLRNKDVIGAFKKVFACSSAQKVATSDA (SEQ ID NO:
 50 477).

ATGACGAACACATCATCCTCTGACTTCACCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG
 CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGGCCGTGACTGCAAAATTTGGT
 CATGATATTCTTGATTGAGGTGGACTCTCGCCTCCACACCCCCATGTACTTTCTGCTCAGTC
 55 AGCTGTCCATCATGGACACCCTTTTTCATCTGTACCACTGTCCCAAACTCCTGGCAGACAT
 GGTTTCTAAAGAGAAGATCATTTCTTTGTGGCCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT
CTGTAACCTCTGAGATACCCAGTCTGATGAACCGCAAGAAGTGTCTTTTGCTGGCTGCT
GGTGCCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC
CTTACTGTGGCTCCCGAAGTATCAACCATTTTTCTGTGAGATCCCAGCAGTTCTGAAACT
5 GGCCTGTGCAGACACGTCCTTGTATGAAACTCTGATGTACATCTGCTGTGCCTCATGTTG
CTCATCCCCATCTCTATCATCTCCACTTCTACTCCCTCATCTTGTTAACCATCCACCGCAT
GCCCTCTGCTGAAGGTCGAAAAAGGCCTTACCACCTTGTTCCTCCCAGTCTTCCACACCCCG
AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCCAGTCCCTTCCACACCCCG
AGCAGGACAAAGTAGTGTACGCTTCTATACCATTTGTACGCCCCATGCTTAATCCTCTCAT
10 CTACAGCCTCAGAAACAAGGACGTCATAGGGGCATTTAAAAAGGTATTTCATGTTGCTCA
TCTGCTCAGAAAGTAGCAACAAGTGCTTAG (SEQ ID NO: 478).

AOLFR255 sequences:

MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKILIHIDSRHTPMYFLLSQLS
15 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH
YPVLMRSKICWLIVAAAWLGGSIDGFLTPVTMQPFCASREINHFFCEVPALLKLSCTDTSAY
ETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT
YVLPHSYHTPEQDKAVSAFYTLTPMLNPLIYSLRNKDVGTALQKVVGRCVSSGKVTF (SEQ
ID NO: 479).

20 ATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCAACG
CCCGTTTCCCTGGCTTCTCTTGGCCCTCATTCTCCTGGTCTTTTGACCTCCATAGCCAGC
AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCATGTACTTCT
25 GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATGTGCCCCAAATGCTG
GTCGACCAGGTGATGAGCCAGAGGCCATTTCTTTGCTGGATGCACTGCCAACACTTCC
TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCCTATGATCGCTAC
GTAGCCATCTGCAACCCTCTGCACTATCCTGTCCTCATGAGCCGCAAGATCTGCTGGTTGA
TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCGTCACCAT
GCAGTTCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTT
30 TGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGATTAT
GATGCTCCTCATCCCTTCTCTGTCTATCTCGGGCTCTTACACAAGAATTCTCATTACTGTTT
ATAGGATGAGCGAGGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCACACATGG
TGTTGTGACGCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCAC
ACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTTACTCCCATGCTCAATC
35 CACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGGTTGTGGGGA
GGTGTGTCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

AOLFR256 sequences:

MGGKQPWVTEFILVGFQVGPALAILLGLFSVFYTLTLLGNGVIFGHIICLDSKLHTPMYFFLSHL
40 AIIDMSYASNNVPKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVMSYDRYVAICHPF
QYTVIMSWRVCTILASTCWIISFLMALVHITHILRPPFCGPQKINHFIQIMS VFKLACAGPRLNQ
VVL YAGSAFIVEGPLCLELVSNLHILSRHLEDPVMGRAADRLTLPAPSHLCMVGLLFGSTMVM
YMAPKSRHPPEEQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:
481).

45 ATGGGAGGCAAGCAGCCCTGGGTACAGAATTCATCCTGGTGGGATTCCAGGTTGGTCCA
GCACTGGCGATTCTCCTCTGTGGACTCTTCTGTCTTCTATACACTACCCCTGCTGGGGAA
TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCCATGTACTTCTCC
TCTCACACCTGGCCATCATTGACATGTCCTATGCTTCCAACAATGTTCCCAAGATGTTGGC
50 AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGACTTTTTTG
TATTTGGCTTTTGTGTTACAGAGTGCCTGATTTTGGTGGTGATGTCCTATGATAGGTATGT
GGCCATCTGCCACCCCTTTCCAGTACACTGTCTATCATGAGCTGGAGAGTGTGCACGATCCTG
GCCTCAACATGCTGGATAATTAGCTTCTCATGGCTCTGGTCCATATAACTCATATTCTGAG
GCCGCTTTTGTGGCCCAAAAAGATCAACCACTTTATCTGTCAAATCATGTCCGTATTCA
55 AATTGGCCTGTGCTGGCCCTAGGCTCAACCAGGTGGTCTATATGCGGGTCTGCGTTCAT
CGTAGAGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACCTGCACATCCTGTGCGCCATCTT

GAGGATCCAGTAATGGGGAGGGCCGCAGACCGACTTACTCTTCCTGCTCCTTCCCACCTTT
GCATGGTGGGACTCCTTTTTGGCAGCACCATGGTCATGTACATGGCCCCCAAGTCCCGCCA
CCCTGAGGAGCAGCAGAAGGTCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC
CCCTTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGGTGCCCTGAAAAGAGTGTTGTGG
5 AAACAGAGATCAAAGTGA (SEQ ID NO: 482).

AOLFR257 sequences:

MESNQTWITEVILLGFQVDPALELFLFGFLLFYSLTLMGNHILGLIYLD SRLHTPMYVFLSHL
AIVDMSYASSTVPKMLANLVMHKKVISFAPCILQTFLYLAFATECLILVMMCYDRYVAICHPL
10 QYTLIMNWRVCTVLA STCWIFSLLALVHITLILRPF CGPQKINHFFCQIMSVFKLACADTRLN
QVVLFAGSFILVGPLCLVLVSYLHILVAILRIQSGEGRRKAFSTCSSHL CVVGLFFGSAIVMYM
APKSSHSQERRKILSLFYSLFNPLNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).

ATGGAAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGGATTCCAGGTGGACCCA
15 GCTCTGGAGTTGTTCTCTTTGGGTTTTCTTGCTATTCTACAGCTTAACCCTGATGGGAAA
TGGGATTATCCTGGGGCTCATCTACTTGGACTCTAGACTGCACACACCCATGTATGTCTTC
CTGTACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG
CAAATCTTGATGCACAAAAAGTCATCTCCTTTGCTCCTTGCATACTTCAGACTTTTTTG
TATTTGGCGTTTGCTATTACAGAGTGTCTGATTTTGGTGATGATGTGCTATGATCGGTATG
20 TGGCAATCTGTACCCCTTGCAATACACCCTCATTATGAACTGGAGAGTGTGCACTGTCCT
GGCCTCAACTTGCTGGATATTTAGCTTTCTCTTGGCTCTGGTCCATATTACTCTTATTCTGA
GGCTGCCTTTTTGTGGCCACAAAAGATCAACCACCTTTTTCTGTCAAATCATGTCCGTATTC
AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCCTATTTGCGGGTTCTGCGTTCA
TCTTAGTGGGGCCGCTCTGCCTGGTGTGCTGCTCCTACTTGACATCCTGGTGGCCATCTTG
25 AGGATCCAGTCTGGGGAGGGCCGCAGAAAGGCCTTCTCTACCTGCTCCTCCCACCTCTGCG
TGGTGGGGCTTTTCTTTGGCAGCGCCATTGTATGTACATGGCCCCCAAGTCAAGCCATTC
TCAAGAACGGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC
CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCCTTTGGAAA
CAGAGATCAATGTGA (SEQ ID NO: 484).

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AOLFR259 sequences:

MGDNQSRVTEFILVGFQLSVEMEVLLFWIFSLLYLFSLLANGMILGLICLDPRLRTPMYFFLSHL
AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVVMYSYDRFVAICHPL
HYTVIMNWRVCTVLAITSWACGFSLLALINLILLRLPFCGPQEVNHFFGEILSVLKLACADTWIN
35 EIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKKAFTSCSSHL CVVGLYFGMAMVVY
LVPDNSQRQKQKILTLFYSLFNPLNPLIYSLRNAQVKGALYRALQKKRTM (SEQ ID NO:
485).

ATGGGGGACAACCAATCACGGGTACAGAATTCATCCTGGTTGGATTCCAGCTCAGTGTG
40 GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTCTTCAGCCTGCTGGCAA
TGGCATGATCTTGGGGCTCATCTGTCTGGATCCCAGACTGCGCACCCCATGTACTTCTTCC
TGTCACACTTGGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA
AAACCTAGTGAAACACAAAAAACTATCTCGTTTCATCTCTTGCAATTATGCAGATGGCTTTG
TATTTGACTTTTGCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAGATTTGT
45 GGGCATCTGCCATCCCCTGCATTACACTGTATCATGAAGTGGAGAGTGTGCACAGTACTG
GCTATTACTTCTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTAAG
GCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCACTTCTTCGGTGAAATTTCTGTCTGTCTC
AAACTGGCCTGTGCAGACACCTGGATTAATGAAATTTTGTCTTTGCTGGTGGTGTGTTT
TCTTAGTCGGGCCCCCTTCTTGTATGCTGATCTCCTACATGCGCATCCTCTTGGCCATCCTG
50 AAGATCCAGTCAAAGGAGGGCCGCAAAAAAGCCTTTTCCACCTGCTCCTCCCACCTCTGTG
TGGTTGGGCTTTACTTTGGCATGGCCATGGTGGTTTACCTGGTCCCAGACAACAGTCAACG
ACAGAAGCAGCAGAAAATCTCACCTGTTTTACAGCCTTTTCAACCCATTGCTGAACCCC
CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCCTTATACAGAGCACTGCAGAAA
AAGAGGACCATGTGA (SEQ ID NO: 486).

55

AOLFR24B sequences:

MPSINDTHFYPPFFLLGLDGLTHIWFSPFCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM
LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLMFFIHMFTGMETVLLVVMAYDRFVAICNP
LQYTMILTINKTISILASVVVGRNLVLTVPFVFLRLPFCGHNIVPHTYCEHRGLAGLACAPIKIN
5 IYGLMVISYIIVDVILASSYVLILRAVFLPSQDVRLKAFNTCGSHVCVMLCFYTPAFFSFMTH
RFGQNIPHYIHILLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCTTCTTCTCCTGCTAGGAATACCAGG
ACTGGACACTTTACATATCTGGATTCTTTCCCATTCTGTATTGTGTACCTGATTGCCATTG
10 TGGGGAATATGACCATTCTCTTTGTGATCAAACTGAACATAGTCTACACCAGCCCATGTT
CTACTTCTGGCCATGTTGTCTATGATTGATCTGGGTCTGTCCACATCCACTATCCCCAAAA
TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT
GTTCTTTATTACATGTTTACAGGCATGGAGACTGTTCTGTTGGTGGTCATGGCTTATGACC
GCTTTGTTGCCATCTGCAACCTCTCCAGTACACCATGATCCTCACCAATAAAACCATCAG
15 TATCCTAGCTTCTGTGGTTGTTGGAAGAAATTTAGTTCTTGTAAACCCCATTTGTGTTTCTCA
TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG
TCTGGCCGGGTTGGCCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT
TCTTATATTATTGTGGATGTGATCTTAATTGCCTCTTCTATGTGCTTATCCTTAGAGCTGT
TTTTCGCCTTCCCTCTCAAGATGTCCGACTAAAGGCCTTCAATACCTGTGGTTCTCATGTCT
20 GTGTTATGCTGTGCTTTTACACACCAGCATTTTTCTTTTATGACACATCGTTTTGGCCAA
AACATTCCCCACTATATCCATATTCTTTTGGCTAACCTGTATGTGGTTGTCCCACCTGCCCT
TAACCCTGTCATTTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTT
GTACAGAAAGAATAA (SEQ ID NO: 488)

AOLFR33B sequences:

MLHTNNTQFHPSTFLVVGVPGLDVHVWIGFPFFAVYLTALLGNHILFVIQTEQSLHQPMFYFL
AMLAGTDLGLSTATIPKMLGIFWFNLGEIAGACITQMYTHICTGLESVVLTVTGIDRYAICNP
LRYSMILTINKVIAILGIVIVRTL VFVTPFTLTLRLPFCGVRIIPHTYCEHMGGLAKLACASINVIY
GLIAFSVGYIDISVIGFSYVQILRAVFHLPADWDLKALSTCGSHVCVMLAFYLPALFSFMTHRF
30 GHNIPHYIHILLANLYVVFPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ
(SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTCAACCCTTCCACCTTCTCCTAGTGGGGGTCCCAG
GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCCTTCTTTGCGGTGTATCTAACAGCCCT
35 TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG
TTTTACTTCTAGCCATGTTGGCCGCACTGATCTGGGCTTGTCTACAGCAACCATCCCCA
AGATGCTGGGAATTTTCTGGTTAATCTTGGAGAGATTGCATTGTTGGTGCCTGCATCACACA
GATGTATACCATTCATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA
GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA
40 TAGCCATTCTGGGCATAGTCATATTGTGAGGACTTTGGTATTGTGACTCCATTACATTT
CTCACCTGAGATTGCCTTTCTGTGGTGTCCGGATTATCCCTCATACCTATTGTGAACACAT
GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCCTTCTCA
GTGGGATACATTGACATTTCTGTGATTGGATTTTCTATGTCCAGATCCTCCGAGCTGTCTT
CCATCTCCCAGCCTGGGATGCCCGGCTTAAGGCACTCAGCACATGTGGCTCTCACGTCTGT
45 GTTATGTTGGCTTTCTACCTGCCAGCCCTCTTTTCTTCTATGACACACCGCTTTGGCCCAA
CATCCCTCATTACATCCACATTTCTTCTGGCCAATCTGTATGTGGTTTTTCCCCTGCTCTTA
ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA
ACCCTAAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTTCCACAACAATTAGTTAGACA
ATAA (SEQ ID NO: 490)

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AOLFR112B sequences:

MKNKTVLTFILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILTLTLLDSHLQTPMYFFLRNFSF
LEISFTNIFIPRVLSITTNKKSISFAGCFTQYFFAMFLGATEFYLLAAMSVDYVAICKPLHYTTI
MSSRICQLIFCSWLGLMAIPTITLMSQQDFCASNRLNHYFCDYEPLLELSCSDTSLIEKVFL
55 VASVTLVTLVLVLSYAFIHKTLKLPQAQRTKAFSTCSSHMIVISLSYSGSCMFMYINPSAKEG
DTFNKGVALLITSVAPLLNPFYTLRNQVQKQPFKDMVKLLNL (SEQ ID NO: 491)

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC
 TCCAGGTGGCAGTTTTACCTTTCTTTTCCTTGCCTATTTACTCAGCATCCTTGGAAATCTG
 ACTATCCTCATCCTCACCTTGCTGGACTCCCACCTCAGACTCCCATGTATTTCTTTCTCCG
 5 GAACTTCTCCTTCTTGGAAATTTCTTCCACAAACATCTTCATTCCAAGGGTCTGATTAGCA
 TCACAACAGGGAACAAGAGTATCAGCTTTGCTGGCTGCTTCACTCAGTATTTCTTTGCCAT
 GTTCCTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC
 ATCTGCAAACCTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATTT
 TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA
 10 GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA
 CTCTCATGTTTCAGACACAAGCCTCATAGAGAAGGTTGTCTTTCTTGTGGCATCTGTGACCC
 TGGTGGTCACTCTGGTGTAGTGATTCTCTCCTATGCATTCAATTATCAAGACTATTCTGAAG
 CTCCCTCTGCCCCAACAAAGGACAAAAGCCTTTTCCACATGTTCTTCCCACATGATTGTCAT
 CTCCCTCTCTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAGAAGGGGAT
 15 ACATTCAACAAGGGAGTAGCTCTACTCATTACTTCAGTTGCTCCTTTGTGAACCCCTTTAT
 TTACACCTTAAGGAACCAACAGGTAAAACAACCCCTCAAGGATATGGTCAAAAAGCTTCT
 GAATCTTTAA (SEQ ID NO: 492)

AOLFR130B sequences:

20 MEGKNQTAPEFIILGFDHLNELQYLLFTIFFLTYICTLGGNVFIHVVTIADSHLHTPMYYFLGNL
 ALIDICYTTTNVPQMMVHLLSEKKIISYGGCVTQLFAFIFVVGSECLLLAAMAYDRYIAICKPLR
 YSFIMNKALCSWLAASCWTCGFLNSVLHTVLTFLHLPFCGNNQINYFFCDIPPLILSCGDTSLNE
 LALLSIGILISWTPFLCIILSYLYIISTILRISSEGRHKAFSTCASHLLIVILYYGSAIFTYVRPISYS
 LEKDRLISVLYSVVTPLNPNVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTCGACCACCTGA
 ATGAATTGCAGTATTTACTCTTCACCATCTTCTTTCTGACCTACATATGCACCTTAGGAGGC
 AATGTTTTTATCATTGTGGTGACCATAGCTGATTCCCACCTACACACACCCATGTATTATTT
 CCTAGGAAATCTTGGCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG
 30 GTGCATCTTCTGTGAGAGAAGAAATCATTTCTTATGGAGGCTGTGTGACCCAGCTCTTTG
 CATTCAATTTCTTTGTTGGCTCAGAGTGTCTCCTCCTGGCAGCAATGGCATATGATCGATAT
 ATTGCTATCTGTAAGCCGTTAAGGTACTCATTTATTATGAACAAGGCCCTGTGCAGCTGGT
 TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTTGCACACCGTTCTGACCTT
 CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTTCTTCTGTGACATACCTCCCTTGC
 35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAACTGGCTTTGCTGTCCATTGGGATCCTC
 ATAAGCTGGACTCCTTTCTGTGCATCATCTTTCTTACCTTTACATCATCTCCACCATCCT
 GAGGATCCGTTCTCTGAGGGGAGGCACAAAGCCTTTTCCACCTGTGCCTCCACCTGCTC
 ATTGTTATTCTCTATTATGGCAGTGCTATCTTACGTATGTGAGGCCCATCTCATCTTACTC
 TCTAGAGAAAGATAGATTGATCTCAGTGCTGTATAGTGTTGTACACCCCATGCTGAATCCT
 40 GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG
 TGGCAGCCACCAGTTTTCTTCTTGATATATAA (SEQ ID NO: 494)

AOLFR142B sequences:

45 MARKDMAHINCTQATEFILVGLTDHQELKMPLFVLFSLIYFTVVGNLGLILLIRADTSLNTPM
 YFFLSNLAFVDFCYSSVITPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLLASMAYDRY
 VAICNPLLYMVVMTGPGICQLVAVPYSYSLMALFHTILTFRLSYCHSNIVNHFYCDDMPLRL
 TCSDFRQKQLWIFACAGIMFISSLLIVFVSYMFHISAILRMHSAEGRQKAFSTCGSHMLAVTIFYG
 TLIFMYLQPSSSHLDTDKMASVFYTVIIPMLNPLIYSLQNKEVKEALKKIIINKN (SEQ ID NO:
 495)

50 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG
 GCCTCACAGACCATCAGGAGTTGAAGATGCCCTCTTTGTGCTATTCTTATCCATCTACCTC
 TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATTAGAGCGGATACAAGTCTCAACA
 CACCAATGTACTTCTTTCTTAGCAACCTAGCTTTTGTGGATTTCTGTTACTCTTCTGTCATT
 55 ACACCCAAAATGCTTGGGAATTTCTTGTACAAACAAAATGTTATATCCTTTGATGCATGTG
 CTACTCAACTGGGCTGCTTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG

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GCCTATGACCGATATGTGGCCATTTGTAACCCTCTATTGTATATGGTTGTAATGACTCCAG
 GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTAC
 ACCATCTCACCTTCCGCCTCTCCTATTGCCACTCCAACATTGTCAACCATTCTATTGTGA
 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT
 5 GCCTGTGCTGGTATCATGTTCAATTCCTCCCTTCTGATTGTCTTTGTCTCCTACATGTTTCAT
 ATTTCTGCCATCCTGAGGATGCATTACAGTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG
 GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCCTCATTTTTATGTACTTACAGCCT
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATTC
 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA
 10 AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

AOLFR171C sequences:

MAEVNIIVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL
 AFVDLCYSSAITPKMMVNFVVERNTIPFHACATQLGCFLTFMITECFLLASMAFYDCYVAICSP
 15 HYSTLMSRRVCIQLVAVPYIYSFLVALFHTVITFRLTYCGPNLNFHYCDDLPLFALSCSDTHMK
 EILIFAFAGFDMISSSIVLTSYIFIIAILRIRSTQGQHKAISTCGSHMVTVTIFYGTLIFMYLPKS
 NHSLDTDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILFLKIRKLY (SEQ
 ID NO: 497)

20 ATGGCTGAAGTTAATATCATTTATGTCACTGTATTCAATCTGAAAGGAATTACCAACCGGC
 CAGAGCTTCAGGCCCCGTGCTTTGGGGTGTITTTAGTTATCTATCTGGTCACAGTGCTGGG
 CAATCTTGGGTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTACTATT
 TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCCTCTGCTATTACACCGAAGATGATG
 GTGAATTTTGTGTGGAACGCAACACCATTCCTTTCCATGCTTGTGCAACCCAACTGGGTT
 25 GTTTTCTACCTTCATGATCACTGAGTGTTTCTTCTAGCCTCCATGGCCTACGATTGCTAT
 GTCGCCATCTGTAGTCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC
 TGGTGGCAGTTCCATATATATACAGCTTCCTGGTTGCCCTCTTCCACACCGTTATCACTTC
 CGTCTGACTTACTGTGGCCAACTTAATTAACCATTTCTATTGTGATGACCTCCCCTTCTT
 AGCTCTGTCTGCTCAGACACACACATGAAGGAAATTCTGATATTTGCCCTTGGCTATCCTA
 30 GATATGATCTCTTCTCTTCCATTGTCTCCTACCTCCTACATCTTTATTATTGCCGCTATCCTA
 AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTTCCACCTGTGGCTCCCATATGGTGA
 CTGTCATATTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAAATCAAATCACTCC
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCCATGTTAAACCCC
 TAATCTATAGTCTAAGGAACAAAGAAGTGAAGATGCCTCAAAGAAAGCCTTGGATAAAG
 35 GTTGTGAAAACCTACAGATATTAACATTTTAAAAATAAGAAAACCTTATTAA (SEQ ID NO:
 498)

AOLFR225B sequences:

MKNRTMFGEFILLGLTNQPELQVMIFIFLTYMLSILGNLTITLTLLDPLHQTTPMYFFLRNFSF
 40 LEISFTSIFIPRLTSMTTGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI
 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYYCDYGPLVELACSDTSILLELMVI
 LLAVVTLMTLVTLVLSYTYIIRTLRIPSAQQRKAFSTCSSHMIVISLSYGSCMFMYNPSAKE
 GGA FNKGIAVLITSVTPLNPFYITLRNQVKQAFKDSVKKIVKL (SEQ ID NO: 499)

45 ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC
 TCCAAGTGATGATATTCTTTCTGTTCCCTACCTACATGCTAAGTATCCTAGGAAATCTG
 ACTATTATCACCTCACCTACTAGACCCCCACCTCCAGACCCCATGTATTTCTTCTCCTCG
 GAATTTCTCCTTCTTAGAAATTTCTTCCATCCATTTTTATTCCCAGATTTCTGACCAGCA
 TGACAACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTGACTCAGTATTTTTTGTCTAT
 50 ATTTCTTGGAGCTACCGAGTTTTACCTCCTGGCCTCCATGTCTTATGATCGTTATGTGGCCA
 TCTGCAAACCTTGCATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACTAGTGTT
 CTGCTCCTGGTTGGGGGATTCTAGCAATCTTACCACCAATCATCTGATGACCCAGGTA
 GATTTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCT
 TGCCTGCTCAGACACAAGCCTCTTGAAGTATGATGGTCATCCTCTTGGCCGTTGTGACTCTC
 55 ATGGTTACTCTGGTGCTGGTGACACTTTCTTACACATACATTATCAGGACTATTCTGAGGA
 TCCCTTCTGCCCAGCAAAGGACAAAGGCCTTTTCCACTGTTCCTCCACATGATTGTCATC

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCTTCTGCAAAAGAAGGAGGTG
CTTTCAACAAAGGAATAGCTGTACTCATTACTTCGGTTACTCCCTTACTGAATCCCTTCATA
TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAAGGACTCAGTCAAAAAGATTGTG
AAACTTTAA (SEQ ID NO: 500)

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AOLFR274B sequences:

MEFVFLAYPSCPETHLSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYYFLGSLSGIEICYTAV
VVPFILANTLQSEKTITLLGCATQMAFFIALGSADCFLLAAMAYDRYVAICHPLQYPLMLTLTL
CVHLVVASVISGLFSLQLVAFIFSLPFCQAQGIEHFFCDVPPVMHVCAQSHIHEQSVLVAAIL
10 AIAVPFLITTSYTFIVAALLKIHSAAGRHRAFSTCSSHLTVVLLQYGCCAFMYLCPSSSYNPKQ
DRFISLVYTLGTPLLNPLIYALRNSEMKGAVGRVLRNCLSQNS (SEQ ID NO: 501)

ATGGAATTTGTGTTCTGCGCTATCCCTCCTGCCCAGAACTGCATATTCTGTCCTTCCTTGG
GGTCAGCCTGGTTTATGGTTTGATCATCACTGGGAACATTCTCATTGTGGTGTCCATTAC
15 ACAGAAACCTGTCTATGCACATCCATGTACTATTTCTGGGAGCCTTTCTGGGATTGAAA
TATGCTACACTGCAGTGGTGGTGGCCCATATCCTGGCCAACACCCTACAGTCAGAGAAGAC
CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTTCTTCATTGCACTGGGCAGTGTGAT
TGCTTCCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTGCCCACCGTTGCAGTA
CCCTCTCCTCATGACATTGACTCTTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC
20 TGTTCCTGTCTTACAACCTGGTGGCCTTCATCTTCTCTGCCATTCTGCCAGGCTCAGGGC
ATTGAGCACTTCTTTGTGATGTGCCACCAGTCATGCATGTTGTTGTGCTCAGAGTCACAT
TCATGAGCAGTCAGTGTGGTGGCAGCCATACTAGCCATTGCTGTGCCTTTCTTCCTCATC
ACCACCTCCTACACCTTCATAGTGGCTGCTCTGCTCAAGATCCACTCGGCTGCTGGCCGCC
ACCGGGCCTTCTCCACCTGCTCTTCCACCTCACTGTGGTGTGCTGCAGTATGGCTGCTGT
25 GCCTTCATGTACCTGTGCCCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTTCATCTCAC
TGGTGTACACATTGGGAACCCCACTGCTCAACCCACTTATCTATGCCCTGAGGAACAGTGA
GATGAAAGGGGCGTAGGGAGAGTTCTTACCAGGAACTGCCTTTCCAGAACAGCTAG
(SEQ ID NO: 502)

AOLFR276B sequences:

MGGFGTNNISSTTSFTLTGFPEMKGLEHWLAALLLLLYAISFLGNILILFIIKEEQSLHQPMYYFLS
LFSVNDLGVSFSTLPTVLAAVCFHAPETTFDACLAQMFFIHFSSWTEFGILLAMSFHDHYVAICNP
LRYATVLT DVRVAHNGISIVRSFCMVFLPFLKRLPFCKASVLAHSYCLHADLRLPWGDT
TINSMYGLFIVISAFGVDSLILLSYVLILHSVLAIASRGERLKTNLNCTVSHIYAVLIFYVPMVSVS
35 MVHRFRGRHAPEYVHKFMSLCTSNALPNLYLHQD (SEQ ID NO: 503)

ATGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG
AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTGCTTTATGCTATTTCTT
CCTGGGCAACATCCTCATCCTCTTTATCATAAAGGAAGAGCAGAGCTTGACCAGCCAATG
40 TACTACTTCTGTCTCTTTTTTCTGTAAATGACCTGGGTGTGCTTTTTCTACATTGCCCACT
GTACTGGCTGCTGTGTGTTTCATGCCCCAGAGACAACCTTTGATGCCTGCCTGGCCAGAG
TGTTCTTCATCCACTTTTCTCCTGGACAGAGTTTGGCATCCTACTGGCCATGAGTTTGTGAC
CACTATGTGGCCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTGTGG
CCCACAATGGCATATCCATTGTCATCCGCAGCTTCTGCATGGTATTCCCACTTCCCTTCTC
45 CTGAAGAGACTGCCTTTCTGTAAGGCCAGTGTGGTACTGGCCATTCTACTGTCTGCATG
CAGACCTGATTGCGCTGCCCTGGGGAGACACTACCATCAACAGCATGTATGGCCTGTTTCAT
TGTCATCTCTGCCTTTGGTGTAGATTCACTGCTCATCCTCCTCTCCTATGTGCTCATTCTAC
ATTCTGTGCTGGCCATTGCCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTC
ACATATCTATGCAGTGTGATCTTCTATGTGCCTATGGTTAGTGTGCCATGGTTTCATCGAT
50 TTGGGAGGCATGCTCCTGAATATGTGCACAAGTTCATGTCTCTTTGTACCTCCAATGCTCT
ACCCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

AOLFR311B sequences:

MDWENCSSLTDFLLGITNNPEMKVTLFAVFLAVYIINFANLGMIVLIRMDYQLHTPMYFFLS
55 HLSFCDLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLSVMAFDYKAIJNP
LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPLLLLSRSDTQV

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NELVLFTVFGFIELSTISGVFISYCYIILSVLEIHS AEGRFKALSTCTSHLSAVAIFQGTLLFMYFRP
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKLKNKILF (SEQ ID NO: 505)

5 ATGGACTGGGAAAATTGCTCCTCATTAAGTATTTTCTCTTGGGAATTACCAATAACCC
AGAGATGAAAGTGACCCTATTTGCTGTATTCTTGGCTGTTATATCATTAATTTCTCAGCAA
ATCTTGGAATGATAGTTTAAATCAGAATGGATTACCAACTTCACACACCAATGTATTTCTT
CCTCAGTCATCTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCAAGATGCTGG
TAGATCTACTTGCCAAGAACAAGTCAATACCCTTCTATGGCTGTGCTCTGCAATTCTTGGT
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTCAAGTGTGCTATCTACT
10 AGGCCATCATCAACCCCTGCTCTATACAGTCAACATGTCTAGCAGAGTGTGCTATCTACT
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTCTTCTGTGATATCCCTCCTCTCTT
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTATTACCGTCTTTGGTTTAA
TTGAACTGAGTACCATTTCAGGAGTTTTCATTCTTATTTGTTATATCATCCTATCAGTCTTG
15 GAGATACACTCTGCTGAGGGGAGGTTCAAAGCTCTCTACATGCACCTCCCACTTATCTG
CGGTTGCAATTTTCCAGGGAAGTCTGCTCTTATGTATTTCCGGCCAAGTCTTCTCCTATTCT
CTAGATCAAGATAAAATGACCTCATTGTTTACACCCTGTGGTCCCATGTTGAACCCCT
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAAGTAAAAATAAAAT
TTTATTTTAA (SEQ ID NO: 506)

20

AOLFR314 sequences:

MEVKNCCMVTEFILLGIPHTGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG
NLSVFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFHFLGSIECLFTVMAYDRFTAICY
PLRYTVIMNPRICVALAVGTWLLGCIHSSILTSITFTLPYCGPNEVDHFFCDIPALLPLACADTSL
25 AQRVSFTNVGLISLVCFLLILLSYTRITISILSIRTTTEGRRAAFSTCSAHLIALCAYGPIITVYLQPT
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHVPES (SEQ ID NO: 507)

30 ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCACACACA
GAGGGGCTGGAGATGACACTTTTGTCTTATTCTTGCCCTTCTATGCCTGCACTCTACTGGG
AAATGTGTCTATCCTTGTGCTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTTCT
TCCTGGGAAACTTGTCTGTGTTTGACATGGGTTTCTCCTCAGTGACTGTGCTGCAAGTGTCT
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT
TCTTCCATTTCTCGGGAGCATTGAGTGTCTTGTGTTACGGTGATGGCCTATGACCGCTTC
ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC
35 TGGCTGTGGGCACATGGCTGTTAGGGTGCAATTCATTCCAGTATCTTGACCTCCCTCACCTTC
ACCTTGCCATACTGTGGTCCCAATGAAGTGATCACTTCTTCTGTGACATTCCAGCACTGTT
GCCCTTGGCCTGTGCTGACACATCCTTAGCCCAGAGGGTGAGCTTCACCAACGTTGGCCTC
ATATCTCTTGTCTGCTTTCTGCTAATCTTTATCCTACACTAGAATCACAATATCTATCTT
AAGCATTTCGTACAACTGAGGGCCGTCGCCGTGCCTTCTCCACCTGCAGTGTCACTCATT
40 GCCATCCTCTGTGCCTATGGGCCCATCATCACTGTCTACCTGCAGCCACACCCAACCCA
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCTTTGAT
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG
CCATGTTCTGAGAGTTAG (SEQ ID NO: 508)

45

AOLFR324B sequences:

MPIANDTQFHTSSFLLLGIPGLEDVHIWIGPFFSVYLIALLGNAAIFFVIQTEQSLHEPMYYCLA
MLDSIDLSTATIPKMLGIFWFNIKEISFGGYLSQMFFHFFTVMESIVLVAMAFDRYIAICKPL
WYTMILTSKIISLIAGIIVLRSLYMPIVFLLLRPFCHRIIPHTYCEHMGIA RLACASIKVNM
FGLGSISL LLDVLLIILSHIRLYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH
50 DIPQYIHIFLANLYVVPPTLNPVIYGVRTKHIRETVLRFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCCTACTTCTTCTTCTGCTGGGTATCCCAGG
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTTCTCTGTGTATCTTATTGCACTCC
TGGGAAATGCTGCTATCTTCTTTGTGATCCAAACTGAGCAGAGTCTCCATGAGCCCATGTA
55 CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGTCTACGGCCACCATCCCAA
ATGCTGGGCATCTTCTGGTTCAATATCAAGGAAATATCTTTGGAGGCTACCTTTCTCAGA

TGTTCTTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC
CGCTACATTGCCATTTGCAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA
GCCTCATTCAGGCATTGCTGTCTGAGGAGCTTGTACATGGTCATTCCACTGGTGTTTCT
CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG
5 GCATTGCCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT
TTCTCTCTTGTTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT
CTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT
GGTGTTATCTTAGCCTTTTCTACACCAGCATTTTTCTCTTTCTTTACACACTGCTTTGGCCAT
GATATCCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTGTTCCCTCCCACCCT
10 CAATCCTGTAATCTATGGGGTCAGAACCAACATATTAGGGAGACAGTGCTGAGGATTTTC
TTCAAGACAGATCACTAA (SEQ ID NO: 510)

AOLFR328 sequences:

15 MALGNHSTITEFLLGLSADPNIRALLFVLFLGIYLLTIMENLMLLVIRADSCLHKPMYFFLSH
LSFVDLCFSSVIVPKMLENLLSQKRTISVEGCLAQVFFVFTAGTEACLLSGMAYDRHAAIRRP
LLYGQIMGKQLYMHLVWGSWGLGFLDALINVLLAVNMVFCEAKIIHHYSYEMPSLLPLSCSDI
SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL
MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTCCTTGGGCTGTCTGCCGACC
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AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGTCTCCATAAGCCCATGTATTTCT
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25 TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA
TGCTGCCATCCGCCGCCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC
CTTGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCCTCCTAGCTG
TAAACATGGTCTTTTGTGAAGCCAAAATCATTACCACTACAGCTATGAGATGCCATCCCT
CCTCCCTCTGTCTGCTCTGATATCTCCAGAAGCCTCATCGTTTTGCTCTGCTCCACTCTCC
30 TACATGGGCTGGGAAACTTCCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCTACCATC
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CTGCAGTGACACTTTACTATGGCTCAGGTTTGTCTCCGCCATCTCATGCCAACTCAGGTTC
CCCCATAGAGTTGATCTTCTCTGTGCAGTATACTGTAGTCACTCCCATGCTGAATTCCTCA
TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAGAACTTTGGAAAAATATT
35 TGCAATATACCAGACGTTGA (SEQ ID NO: 512)

Claims:

1. A method for representing sensory perception of one or more odorants comprising:
 - 5 (a) providing a representative class of n olfactory receptors or ligand-binding domains thereof;
 - (b) measuring values X_1 to X_n representative of at least one activity of the one or more odorants selected from the group consisting of binding of the one or more odorants to the ligand-binding domain of at least one of the n olfactory receptors, activating at least one of the n olfactory receptors with the one or more odorants, and blocking at least one of the n olfactory receptors with the one or more odorants; and
 - 10 (c) generating a representation of sensory perception from the values X_1 to X_n ;
- 15 wherein at least one of the n olfactory receptors has an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169,
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5 NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO:
511.

2. The method of Claim 1, wherein at least one of the olfactory receptors
specifically recognizes the odorant, and there are between 5 and 350 of the n olfactory
10 receptors selected from the listed amino acid sequences.

3. The method of Claim 1, wherein at least two different activities are measured
to provide the values X_1 to X_n .

15 4. The method of Claim 1, wherein each odorant receptor is expressed in cells,
and the cells expressing each odorant receptor are located at an identifiable position.

5. The method of Claim 1, wherein at least one olfactory receptor is soluble, and
binding of odorant to a ligand-binding domain of the soluble olfactory receptor is
20 measured in solution.

6. The method of Claim 1, wherein at least one olfactory receptor is in solid state,
and binding of odorant to a ligand-binding domain of the solid-state olfactory receptor
is measured on a substrate.

25 7. The method of Claim 1, wherein the value measured for binding is above a
preset limit for specific binding to olfactory receptors.

8. The method of Claim 1, wherein the value measured for activating an olfactory
30 receptor is derived from a signal selected from the group consisting of intracellular
 Ca^{2+} , cAMP, cGMP and IP3.

9. The method of Claim 1, wherein the value measured for activating an olfactory receptor is above a preset limit for specific activation.
10. The method of Claim 1, wherein the value measured for blocking an olfactory
5 receptor is at least a reduction in binding of the odorant or activation by the odorant.
11. The method of Claim 1, wherein the representation of sensory perception is generated with a neural network.
- 10 12. A biosensor comprised of the n ligand-binding domains or olfactory receptors of Claim 1.
13. A method for producing a database of odorant representations comprising:
(a) providing one or more known odorants and
15 (b) generating a representation of the one or more known odorants in accordance with the method of Claim 1 to produce the database.
14. A database produced by Claim 13.
- 20 15. A method of identifying an unknown odorant comprising:
(a) measuring values X_1 to X_n representative of at least one activity selected from the group consisting of binding the unknown odorant to a ligand-binding domain of at least one of n olfactory receptors, activating at least one of n olfactory receptors with the unknown odorant, and blocking at
25 least one of n olfactory receptors with the unknown odorant;
(b) generating a representation of the unknown odorant from the values X_1 to X_n ; and
(c) comparing the unknown odorant's representation to the database of Claim 14 to identify the known odorant which is most similar in
30 representation.
16. A method of producing an artificial odorant comprising:

- 5 (a) measuring values X_1 to X_n representative of at least one activity selected from the group consisting of binding a desirable odorant to a ligand-binding domain of at least one of n olfactory receptors, activating at least one of n olfactory receptors with a desirable odorant, and blocking at least one of n olfactory receptors with a desirable odorant;
- (b) generating a representation of the desirable odorant from the values X_1 to X_n ;
- 10 (c) decomposing the desirable odorant's representation into representations of known odorants from the database of Claim 14 or superposing known odorants' representations from the database to reproduce the desirable odorant; and
- (d) formulating the known odorants to reproduce sensory perception of the desirable odorant and thereby produce the artificial odorant.

15 17. An artificial odorant produced by Claim 16.

18. A method of identifying a primary odorant related to sensory perception comprising:

- 20 (a) providing a representative class of n olfactory receptors or ligand-binding domains thereof,
- (b) measuring at least one activity of a odorant selected from the group consisting of binding of the candidate odorant to the ligand-binding domain of at least one of the n olfactory receptors and activating with the candidate odorant at least one of the n olfactory receptors, and
- 25 (c) identifying the candidate odorant as a primary odorant if only one or less than 10% of the representative class of n olfactory receptors is bound or activated;

wherein at least one of the n olfactory receptors has an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID

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19. A primary odorant identified by Claim 18.

20. A method of identifying a compound which blocks activation by a odorant of at least one olfactory receptor comprising:

- 25 (a) producing a structurally-related candidate compound from a ligand of the at least one olfactory receptor,
- (b) measuring activation by the odorant of the at least one olfactory receptor with the candidate compound, and
- (c) identifying the candidate compound as a compound which blocks activation if activation of the at least one olfactory receptor is reduced or
- 30 inhibited;

wherein at least one of the olfactory receptors has an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID

NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID
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25 21. The method of Claim 20, wherein the ligand is a primary odorant.

22. A compound which blocks activation of an olfactory receptor identified by Claim 20.